

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:06:22 ; Search time 48 Seconds
(without alignments)
1336.590 Million cell updates/sec

Title: US-09-874-162a-8
Perfect score: 4078
Sequence: 1 MTGIAAASFNTGRFGCG.....KALFTDVSQVSKSKQKL 776

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1127.5	27.6	947	2	US-09-270-767-45347, A Sequence 45347, A
2	987.5	24.2	835	2	US-09-270-767-60845, A Sequence 60845, A
3	661	16.2	243	2	US-10-144-198-16 Sequence 16, Appl
4	661	16.2	243	2	US-10-104-047-2404 Sequence 2404, Ap
5	437.5	10.7	102	2	US-09-513-999C-7263 Sequence 7263, Ap
6	238.5	5.8	604	2	US-09-339-947A-8 Sequence 8, Appl
7	224	5.5	611	2	US-09-339-947A-1 Sequence 1, Appl
8	211	5.2	243	2	US-09-270-767-44285 Sequence 44285, A
9	160	3.9	1401	2	US-08-755-587-186 Sequence 186, App
10	159	3.9	1494	2	US-08-755-587-186 Sequence 186, App
11	156.5	3.8	3696	2	US-09-134-001C-5080 Sequence 5080, Ap
12	153.5	3.8	1279	2	US-09-710-279-3188 Sequence 3188, Ap
13	153.5	3.7	584	2	US-09-248-796A-17551 Sequence 17551, A
14	150	3.7	912	1	US-07-789-915A-8 Sequence 8, Appl
15	150	3.7	912	1	US-08-005-002C-8 Sequence 8, Appl
16	150	3.7	912	1	US-08-487-203A-8 Sequence 8, Appl
17	149	3.7	1087	2	US-09-830-230A-322 Sequence 322, App
18	149	3.7	1119	2	US-09-830-230A-321 Sequence 321, App
19	146.5	3.6	1235	1	US-08-118-101A-2 Sequence 2, Appl
20	142.5	3.5	1972	2	US-09-418-710-21 Sequence 21, Appl
21	142.5	3.5	1972	2	US-09-839-479-21 Sequence 21, Appl
22	139.5	3.4	2446	2	US-09-949-016-11439 Sequence 11439, A
23	137.5	3.4	2954	2	US-09-150-867-1 Sequence 1, Appl
24	135	3.3	3210	2	US-09-538-092-1154 Sequence 1154, Ap
25	135	3.3	3248	1	US-08-353-700-1 Sequence 1, Appl
26	135	3.3	3248	4	PCT-US95-16216-1 Sequence 1, Appl
27	133	3.3	472	2	US-09-248-796A-20611 Sequence 20611, A

28	132	3.2	2482	1	US-08-328-254-6 Sequence 6, Appl
29	131.5	3.2	4377	2	US-09-949-016-6978 Sequence 6978, Ap
30	131	3.2	1147	2	US-09-538-092-1074 Sequence 1074, Ap
31	131	3.2	1602	2	US-09-269-874A-7 Sequence 7, Appl
32	131	3.2	1621	2	US-09-269-874A-5 Sequence 5, Appl
33	131	3.2	1639	2	US-09-269-874A-3 Sequence 3, Appl
34	130.5	3.2	3913	2	US-09-949-016-10933 Sequence 10933, A
35	130	3.2	2375	2	US-09-538-092-1131 Sequence 1131, Ap
36	129.5	3.2	614	2	US-09-248-796A-17642 Sequence 17642, A
37	129	3.2	1164	2	US-09-538-092-399 Sequence 399, App
38	128.5	3.2	907	2	US-08-938-830-26 Sequence 26, Appl
39	128.5	3.2	907	2	US-09-020-222-26 Sequence 26, Appl
40	128.5	3.2	907	2	US-09-068-377-26 Sequence 26, Appl
41	128.5	3.2	1167	2	US-10-274-409-2 Sequence 2, Appl
42	128.5	3.2	1167	2	US-09-803-671B-2 Sequence 2, Appl
43	128.5	3.2	1712	2	US-09-949-016-9450 Sequence 9450, Ap
44	128	3.1	798	2	US-09-203-453-5 Sequence 5, Appl
45	128	3.1	798	2	US-09-900-236-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-270-767-45347
; Sequence 45347, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45347
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45347

QY	65	MTDAARBOESLKKKIQPKSLTSSVSNGV---STPRHSGSLTPVTPPTPSS	120	Query Match 27.6%, Score 1127.5; DB 2; Length 947; Best Local Similarity 32.9%, Pred. No. 4.7e-96; Matches 273; Conservative 137; Mismatches 240; Indels 179; Gaps 26;
DB	1	MAPAKKREKOS-----NPDGSAANGIIIGLTGAPASNAGSTVPPTAGQVLTN	49	
QY	121	SFRSTP-----TEPTQIVRPLRTMLAPRPHRTLTWHSNRPNIKRTKPKVDUM	174	
DB	50	GHOQOELFLQAFKPPQIYKRLNHRHTNPIFLNRLTSTYKEMSRNKRKRI5FOVNSM	109	
QY	175	LSKVEKMKGEESHLSA-HLQLTFTGFPHKNDKPSNSNEQ-----NSVTLT	222	
DB	110	LEST-----TQKSAVAVQNTYHVIYDLSHETLPRALDNESGEDLLQROLCCEABSVYE	164	
QY	223	VLVKVCVKRKRKQVSCIRQVPTGKKOVLPLIDINQTKPGNPSLAVSNNEFP-SNSHM	281	
DB	165	TTLVKIRSRKQSTLFOELSKSQIVNVP---KRVGHAHTISIPLOTRMGEQHT	221	
QY	282	VKVSILFLRVTRPRRRFNGINTEMENTDUNELPARRRNDEDEKTFVAQMTYFDK	341	
DB	222	L-VKYLFRIR-----VLSPTON--DENNETP-NKRSHPN-EKMFSELTILEK	266	
QY	342	NRRLQLDGEYEVAMQMEBCPI---SKKATWETIIDGKRLP---PFETFSQPTLOFT	395	
DB	267	SSGP-ITGEYEAALQPLNSTRSISFSPKCTWETMD-SYPLSLTYDVYQOSPMUKFH	324	
QY	396	LRTWGEYNDKSTAPIALPSTR-----NSESILHOEN-----KPGSKVPTQTI	437	
DB	325	LTL---SNEQLPEMISAPELQRYVYVHDAVAEMNNYNNNNNNNCGSLKNGSGGNSV	381	

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Qy 438 AWKESLTTDLQRRKEKDPFENRROKRLRYOPOLYNNNTGQOFARBDLHCPOWTLNCRKJ 497
Db 382 C-----KTP-----EHIQIYNNFNTSNNTQOQIETTYTOELNCPWGLDOLKRL 423
Qy 498 YSLKHLKLCIHSRPIFNYYVYHFKCARIDVINECYGSAYNQDILHROGFAFSBN-GF 556
Db 424 YALLHLKLCIHSRPFYTYGAGSGARIDVTINDAYDVGSAVYDLAGPSSGSAFTCCG 483
Qy 557 VKRPIYTHILVLRPKPKTKASMSFLESEGEVEOQOTYSSGHNRLYFHSDTCLPLRQEM 616
Db 484 VRTSVTSLSLMWCRPRROKCLDBEFLDLDEISNORSYITGNHRLYHHTETCLPVPARKEL 543
Qy 617 EYDSEDEKDPFWLREKTIQIIEEFSVYNGEKEVMLKMLYLVKKGFIADNQNTHACMLF 676
Db 544 DIDSGESDEPLMLRQKTIOMIDBFSDVNGEKEMLKMLYLVKRRHGFVGDCQPLIACENF 603
Qy 677 VENTYQKIIKKNLCENFMILHVSMDFNLSIMSIDKAYTKLRMOOKLEKES----- 730
Db 604 LDKKTEIYRKULYNNFILHMCSLPRFYGLIAETVKKYQKLGGLSKYAAOGLMQROR 663
Qy 731 -----ASPANEITE----- 740
Db 664 EEQLKYMLDVGMHKKQEDPKTLKSPQKPAPPADQASTSASTSGSGSSGSMQPPKMPA 723
Qy 741 -----EONGTANGFSEINSKREKALETDSVSGVSKSKKQKL 776
Db 724 HLKRGSAASSPGVQSGKTENGNGSNS-----SSNSKUNVAKKSADQPL 767

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RESULT 2
US-09-270-767-60845
; Sequence 60845, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60845
; LENGTH: 835
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-60845

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Query Match          24.2%; Score 987.5; DB 2; Length 835;
Best Local Similarity 33.3%; Pred. No. 4, 9e-83;
Matches 233; Conservative 119; Mismatches 194; Indels 153; Gaps 22

QY      QESHSLA-HIQLTFTGFPHKNDKSPENSENQ-----NSVTLEVLAVYCHKK 232
      : : : : :
Db       3 QKSEAVSONYLIVHIVYDLSLHEKIPARLDNDSGEDLLQEQULLCEAGSVSVETLLVYITRSK 62
QY      RKDVSCPIROVPTGKKOVPILPDLNQTGRGNPSLAVSNBEP--SNSMVMKSYSLPLPV 291
      : : : : :
Db       63 RKDSTFLDFOELSLKSCSQIVNYP--KDRGGEHATISIPQTMRPMGEHTL--YKLLFRI 117
QY      TRPGRFRBFNGMNGETNENIDVNEELPARKKRENDGEKTFVAQMTVPDKNRRLQDLDOE 351
      : : : : :
Db       118 K-----VLSPTCN--DENAEPRP-NKKSRRP-KEMFOSELILYEKSGF-ITEGE 163
QY      YEVAHQMBEBCI---SKKRATWETILLDCKLP---PFTFSGQPILOTLAMTGETNDK 405
      : : : : :
Db       164 YEAMIQPINSTSIKSFSPKCKTWTMPD-SYPLSLIYDVYQSQSPMLKHTLL--SNEQ 219
QY      STAPIAKPLATR-----NSESILHOEN-----KPGSVKPTOTIAKESITLTDL 447
      : : : : :
Db       220 LPKMSISBELQYVGHDLVALEMVNNNNNNNNNNNNNNNSGLKNGSGGNSIVC----- 270
QY      QTRKEKQDTPNENRQKRLIFPYQFLVNNNTTQOTTEARDLHCPMCTLNCRKLYSLHKLKIC 507
      : : : : :

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[illegible]

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RESULT 3
US-10-144-198-16
; Sequence 16, Application US/10144198
; Patent No. 6833247
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies Inc
; TITLE OF INVENTION: Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 105 R1
; CURRENT APPLICATION NUMBER: US/10/144,198
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 16
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-198-16

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Query Match      16.2%; Score 661; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1  MTGIAASFANTCRFGCGCGLHPPTLADLIHIEDNHIDTPRYLKEKOLQOPTVALSY 60
Db      1  MTGIAASFNTCRFGCGCGLHPPTLADLIHIEDNHIDTPRYLKEKOLQOPTVALSY 60
QY      61  INRMETDAARREOESLKKKIQPKLSTLTSSSVSGNVSTPPRHSGSLTPVPPTPTSS 120
Db      61  INRMETDAARREGSLKKKIQPKLSTLTSSSVSGNVSTPPRHSGSLTPVPPTPTSS 120
QY      121  SFRSSTPT 128
Db      121  SFRSSTPT 128

RESULT 4
US-10-104-2404
; Sequence 2404, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:

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PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2404
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2404

Query Match 16.2%; Score 661; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGIAAASFNTGCGGCGHFPPLADLIEHIEDNHIDTPRVLEKQLOOPTVALSY 60
DB 1 MTGIAAASFNTGCGGCGHFPPLADLIEHIEDNHIDTPRVLEKQLOOPTVALSY 60
QY 61 INREMTDAARREOESLKKKIOPKLSLTLSXSVSRGVSTPPRHSSGSLTPPTPTPSS 120
DB 61 INREMTDAARREOESLKKKIOPKLSLTLSXSVSRGVSTPPRHSSGSLTPPTPTPSS 120
QY 121 SFRSSTPT 128
DB 121 SFRSSTPT 128

RESULT 5

US-09-513-999C-7263
Sequence 7263, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7263
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 27
OTHER INFORMATION: Xaa=Ala or Asp
FEATURE:
NAME/KEY: UNSURE
LOCATION: 32
OTHER INFORMATION: Xaa=His or Asn or Arg or Ser
FEATURE:
NAME/KEY: UNSURE
LOCATION: 36
OTHER INFORMATION: Xaa=Asp or Asn
FEATURE:
NAME/KEY: UNSURE
LOCATION: 41
OTHER INFORMATION: Xaa=Asp or Gly
FEATURE:
NAME/KEY: UNSURE
LOCATION: 79
OTHER INFORMATION: Xaa=Lys or Thr
FEATURE:
NAME/KEY: UNSURE
LOCATION: 83
OTHER INFORMATION: Xaa=Lys or Arg
FEATURE:
NAME/KEY: UNSURE

LOCATION: 89
OTHER INFORMATION: Xaa=Ser or Tyr
US-09-513-999C-7263

Query Match 10.7%; Score 437.5; DB 2; Length 102;
Best Local Similarity 89.1%; Pred. No. 5e-33;
Matches 90; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 MTGIAAASFNTGCGGCGHFPPLADLIEHIEDNHIDTPRVLEKQLOOPTVALSY 60
DB 1 MTGIAAASFNTGCGGCGHFPPLADLIEHIEDNHIDTPRVLEKQLOOPTVALSY 60
QY 61 INREMTDAARREOESLKKKIOPKLSLTLSXSVSRGVSTP 100
DB 61 INREMTDAARREOESLKKKIOPKLSLTLSXSVSRGVSTP 101

RESULT 6

US-09-339-947A-8
Sequence 8, Application US/09339947A
Patent No. 6630616
GENERAL INFORMATION:
APPLICANT: YOSHIDA, No. 6630616umasa
APPLICANT: YANAI, Yukihiko
APPLICANT: KATO, Yoshihiro
APPLICANT: HIRATSUKA, Junzo
APPLICANT: TAKAHASHI, Shigeru
APPLICANT: MIYA, Tatsushi
TITLE OF INVENTION: GENE FOR FLORAL REGULATION AND METHODS FOR CONTROLLING
FILE REFERENCE: 032735-001
CURRENT APPLICATION NUMBER: US/09/339, 947A
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: JP 1998-180065
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: JP 1999-179043
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 604
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: ZN PING
LOCATION: (310)..(335)
US-09-339-947A-8

Query Match 5.8%; Score 238.5; DB 2; Length 604;
Best Local Similarity 18.9%; Pred. No. 3.9e-13;
Matches 130; Conservative 95; Mismatches 242; Indels 221; Gaps 22;

QY 129 EPTQIYRFLRLRLIADIFLHRLTYNSH--RNSRTNI-----KRTFKVDDMLSKVE 179
DB 27 KPVLYNIIQRRSIXONPAFLORCLLYKHARRKRSITISLSGCTKKELRQAQIIFPLYV 86
QY 180 KMKGEQESHLSAH-----LQLTGTFPKNDKPS---PNSN--EQNSVTLAV 223
DB 87 LLAAPTNNVSLBGSPYRPSRACLTSFHEFGKDYTAATPVLPDVKNATSRACSLNI 146
QY 224 LVVVCVHKRR--DVSCPIROYPTGKQ-----VLUYDLNQTGRGNPPLAVS 270
DB 147 ILIS-CGRAQCTPDNNCSGNHYBGLTQLGKGCFFGKIP--DLAASSLGNCSLSL- 202
QY 271 SNEFEPNSHMVXSYSLFVYTRPGRRFNGMNGETNENIDVNEELPA--RRKRNEDG 328
DB 203 -----GHTVMSSTVEMTPSFLPKFLBDS 228
QY 329 EKPTVAGMTVFDKRRRLQLLDGEYVAMQEMECPIISKRAATWETITLDGRLPFFETFSQ 388
DB 229 CLTFCGQVDATGSPQLQVSIISAQEGAKQMSSPYS-----VYSYNDVPP----- 274
QY 389 GPTLQPTLRWTGETNDKSTAPIAKPLATRNSESLHGENKPGSVKPTQTIAVKSLTTDLQ 448

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Db 275 -----SSLTHTIR 282
QY 449 TRKEKOTPENRQKRIFFQFLYNNTRROOTEARDDLHCPCWCTLNCRKLYSLKLKHLKCH 508
Db 283 LBSG-----NVLNRYKYNTNTMKTETVEDFCPCFLVPGSGFKGLCHLNASH 331
QY 509 SRPFYVYVHPKCARIDVSI-NECYDGSYAQNPDJHROGFAFSNGPVRKPTPT- 563
Db 332 DLFHYFYMISEGQAVNSLKTDSWRTLLABGVDRHQTFSYRSFKKRVKVEISSDKI 391
QY 564 ----HILVC-RPKRTKMSSEFLESEDEVEQORTYSSGH----- 598
Db 392 RHVHPHIVDGSPEDAQ-----SEDDYVQRENGSSVAHASVDPANSLSGNSLAPTY 445
QY 599 -----NRLYFSDTCLPLRPOEM--EVDSEDEKDEPMLEKREKT 633
Db 446 LQFGKTRKLSVERADPRNQLQKQPFHSHRAQPMASKVPSDRSDEBDDIADPFED 505
QY 634 ITQIEFSDVNEGEKEVMKLMNLHVKGFIADNONHACMLFVENYGOKIIRKNL---C 690
Db 506 RMDLDFVUTYDEKLIEMMNSFVRKQVLAUGHIPWACEAFSPHGGELVQNPALLMC 565
QY 691 RNFMLHLVSMHDFNLISIMSIDKAVTKL 718
Db 566 WRFF--MVKLMNHSLDADAMNACNTIL 591

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RESULT 7

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US-09-339-947A-1
; Sequence 1, Application US/09339947A
; Patent No. 6630616
; GENERAL INFORMATION:
; APPLICANT: YOSHIDA, No. 6630616umasa
; APPLICANT: YAMAI, Yukihito
; APPLICANT: KATO, Yoshihiro
; APPLICANT: HIRATSUKA, Junzo
; APPLICANT: TAKAHASHI, Shigeru
; APPLICANT: MIWA, Tatsushi
; TITLE OF INVENTION: GENE FOR FLORAL REGULATION AND METHODS FOR CONTROLLING
; TITLE OF INVENTION: FLOWERING
; FILE REFERENCE: 032735-001
; CURRENT APPLICATION NUMBER: US/09/339,947A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: JP 1998-180065
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: JP 1999-179043
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 611
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: ZN FING
; LOCATION: (306)..(327)
US-09-339-947A-1

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Query Match 5.5%; Score 224; DB 2; Length 611;
Best Local Similarity 19.1%; Pred. No. 9e-12;
Matches 132; Conservative 102; Mismatches 252; Indels 206; Gaps 23;

QY 129 EPPQIYRPLKTRMLPIPLHRTLYTMSHRNSTNKKRTFKYKDDMLSKYKKGQESH 188
Db 27 KPELNIITIIQRRIRNPLFLQRCILHYKLEAKHRRILQMTVFL-----SG 70
QY 189 SISAHQLTFTGFFHKDKSPNSENONSVTLEVLIVKVCCHKRQDVSCPIRQ----- 242
Db 71 AIDAGQ-----TQGLFLYIILARIVSPK-----PAVEYSAVVR 105
QY 243 ----VPTGKKQVP-----LIPDLN-----QTRGN-----FSLAVSSNEFEPSNSH 280

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Db 106 FSRACILTGLGVDSVQAQANFLPDMNRRLALEAKSGLALILFISFAGAONSQEGIDSG 165
QY 281 MVKSYSLFRTYTRPRRRREFNGINGETNENIDVNEELPARRRKRNDEDEKTFVAQWTVVD 340
Db 166 KHS-----GNIGHC-----LMSKIFLQ-----SLYASQ 191
QY 341 KNRRLLQLDGEYEVAMQEMEBECPIKRAWTETLLDGRKLPPFTFSOGPTLQFLRWTG 400
Db 192 KSPNNDLQGRVDTVLVENQPCFILTMSSEKCVS-----IQVSPNPLT----- 236
QY 401 ETNDKSTAPIAKPLATRNSESLHQNKPQSVKPTOTIAVKSLLTTDLQTRKEDTPNEKR 460
Db 237 ----SSSPQVQVITISABEVGSTEKSPYSFYSNDIS--SSSLQIIRLR-----TGN--- 283
QY 461 QKLRIFYOFLYNNTRROOTEARDDLHCPCWCTLNCRKLYSLKHLKCHSRPIFYNYVHPK 520
Db 284 ----VVENRYNNKLOKTEVTEDESCPCFLVKCASFKGLRHLDPSTHDLNFEFWYIE 339
QY 521 GARIDVINECYDGSYAQNPDJH-ROGFAF-----SRNGP----- 556
Db 340 PQAVNVSLKTEBTMISKV-NEDDVPKQOTFFFSKKFRRRROKQSVRSRQGFHLGLGE 398
QY 557 -VKRTPTIHLVCRKR-----TKA 575
Db 399 YLDKTDADHSVRSSEKRIIPGKHRYRIGAESGQRPVPGTSPADYVQSGDPDYVSIAGS 458
QY 576 SMSSEFLESEDEVEQO--RTYSSGHNRLYFHSDTCLPLRPOEM--EVDSEDEKDEPMLE 631
Db 459 TMLQPAKTRKISIESDLRNSLLQKQPFHSHRAQPMALBEVLSDRSDEBDDIADVADF 518
QY 632 KTIQIEFSDVNEGEKEVMKLMNLHVKGFIADNONHACMLFVENYGOKIIR-KNLIC 690
Db 519 EDRMLDPEVDYTKDEKQMMHMSFVRKQVLAUGHIPWACEAFSRHLGPIMVTPHIL 578
QY 691 RNFMLHLVSMHDFNLISIMSIDKAVTKLRQEMO 722
Db 579 WCMRVFMVKLMNHGLDARTMNCNTFLBQLQ 610

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RESULT 8

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US-09-270-767-44285
; Sequence 44285, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44285
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44285

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Query Match 5.2%; Score 211; DB 2; Length 243;
Best Local Similarity 26.7%; Pred. No. 3.3e-11;
Matches 69; Conservative 49; Mismatches 98; Indels 42; Gaps 11;

QY 104 SSGSLTPPYTPITSSSFSSSTP-----TEPTQIYRPLKTRMLPIPLHRTLYTMSH 157
Db 3 MNGSTVPPRABEQVNLNGHQOQELFLQAFKFTQIYRLRHRHETNPFLFARTLSYMK 62
QY 158 RNSRTNIRKRTKPVDDMLSKYKKGQESHSLA-HLQLTGFFHKDKSPNSENO 216
Db 63 RNSRNKRKISFQVNSMLESI-----TQKSEAVSONYLVIVYDSLHEKLPARLDNMSGD 117
QY 217 -----NSVLEVLIVKVCCHKRQDVSCPIRQVPTGKKQVPLIPDLNQTGRGNP 265
Db 118 LIQOELLCEAGSVSVETTLTKITRSKRKDSITLDPQELLSKCSQIVY--NSKDRVGEHA 174

```

QY 266 SLAVSSNEEP-SNSHMVYSLLFRVTRPGRRFNGMNGTENTENIDVNEELPARRKN 324
DB 175 TISIPLOTRPMGEQHTL--YKLLPRIK-----VLSPTCN--DENATPP-NKRS 220
QY 325 REDGEKTFVAMQTVFDKN 342
DB 221 RPN-EKMFSEELIYKRS 237

RESULT 9

US-09-750-590A-2
; Sequence 2, Application US/09750590A
; Patent No. 6780987
; GENERAL INFORMATION:
; APPLICANT: Herman, Ira
; APPLICANT: Welch, Alice
; TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL AND
; TITLE OF INVENTION: ABNORMAL CELL MIGRATION
; FILE REFERENCE: TUI-001CP
; CURRENT APPLICATION NUMBER: US/09/750,590A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/170,182
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 09/733,818
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1401
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-750-590A-2

Query Match 3.9%; Score 160; DB 2; Length 1401;
Best Local Similarity 18.8%; Pred. No. 3.4e-05;

Matches 135; Conservative 139; Mismatches 285; Indels 160; Gaps 30;

QY 36 NHIDDP--VLEKQELQOPTYVALSYINRPMTPAARBOESLKKIOPKSLTSSSV 92
DB 719 NNLTTEMGNVPLKVEBKSHDVAVDLNTKLSVTHKYTE--KLEMEKLMENNSL 775
QY 93 SRGNVS-----TPRRSSG--SLTPPVTPITSSSRSSSTPEPTQIYRFLTRNLI 143
DB 776 SK-NVSRLETVFIPERHEKEMALKNITELKQSLKCGDQEKIYSLMSENNDL 834
QY 144 APIFLHRLTYMSHNSNTNKKRTFKYDDMLSKYERKKGESLSLAHLQLTGTGFH 203
DB 835 KKTMSHQVVPVKTHEITLSTLDTKTNRELVDYK-KCED-----INQEFVKIKD 885
QY 204 KNDKPSSENEONSVTLEVLVAVCHKKRDVSCPIROVPTG-----KKQVPLIPD 255
DB 886 ENELIKRLLENQONVAKAYISLRHEKMSGLRSMKKVQNSAELIAKTKSSEBYVT 945
QY 256 LNQTKPGNPSLAVSSNEFEPNSHMVYSLLF-----RVRTRGRREFGMNGETNE 309
DB 946 LHE-----BIAQKRELDTIOECIKLKVAPIISLEECERFKATEKELKQLSQOTQK 998
QY 310 NIDVNEELPARRKRRREDGEKTFVAMQTVFDK-----NRRLQLL 348
DB 999 YNTSEEEKKCKCKQENDKLLKELLTLQKDLKDKNVIENSYETERALSRKTEBLNQLDL 1058
QY 349 DGEYEVANQEMEECPISISKRAIWE-----TIDGKRLPPFETFSOGPTLOFLRWGTEN 403
DB 1059 LOKTTEAKKEKEKVLVEBAKQSEILAAQTLQKQHP-----LEQVESLKSLSTIET- 1113
QY 404 DKSTAPLAKPLATRNS-----ESLHQENKPGSVKPTQTIIVAKESITDDL----- 447
DB 1114 -----LKEELTKQRCYEKEQOVTQRLQMLENQNSSVPLAHLQVKEAFBKVGIIIX 1167
QY 448 QTRKEKQTPNENR-----OKRIFVQPLVNNNTRQ-----QTEARD-----DLHCP 488
DB 1168 ASLRKEBESQNKTEBVSRLQSEIQ-----NTKQALKLLETRVVDLSKRYKATYSDLTQ 1222

QY 489 WCLINCRKLYSL-LKHLKLCBSRFIFENYVYHPKGARIDVINSINECYDSYAGNPDIHQP 547
DB 1223 ISDLN-EKLANINRYEVSCE-----VLHAK--KKGLSADBEKELHFSIEGELHXQ- 1272
QY 548 GPASRNGPVKRTPTTHILVCPKTKASMSFLESED-----GEVQOHTYSSGHR 600
DB 1273 -----QERCKSLITTTTEL-----QRRIOESAKQ-IEAKNKITTELLNDVRLKQALNGLSQ 1323

RESULT 10

US-08-755-587-186
; Sequence 186, Application US/08755587
; Patent No. 6045397
; GENERAL INFORMATION:
; APPLICANT: Futreal, Phillip A
; APPLICANT: Wooster, Richard F
; APPLICANT: Ashworth, Alan
; APPLICANT: Stratton, Michael R
; TITLE OF INVENTION: Materials and methods relating to the
; TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
; TITLE OF INVENTION: susceptibility gene and uses thereof.
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson
; STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
; CITY: Raleigh
; STATE: NC
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,587
; FILING DATE: 25-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9523959.6
; FILING DATE: 23-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525555.0
; FILING DATE: 14-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9617961.9
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-135
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1494 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-755-587-186

Query Match 3.9%; Score 159; DB 2; Length 1494;
Best Local Similarity 18.3%; Pred. No. 4.7e-05;

Matches 177; Conservative 151; Mismatches 355; Indels 284; Gaps 46;

QY 23 FPLADLIEHIDNHIDTPRVLKQELQOPTYVA-LSYINRPMTPAARBOESLKKKIQ 81
DB 370 FKIASNKIEIKSENIRKSKMLFPOIDEBHYTNLACLEIYVTSLSQKPKSKS--HALD 427
QY 82 PKSLTILSSSVSRBNVTPRRHSGSLPPPTPTTSSSRSSSTPEPTQI----- 133
DB 428 FOINI-ISGFVQ--NSTYVSDSGHTAPPLSLKQDPDSRNRLTPQKAITELSTILE 484
QY 134 -----YRFLTRNLADIPLHRLTYMSHNSRT--NIKRTFKYDDM-----LSKVE 179

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Db      485  BSGSGQEFPTQFRK---PSHIQKNPMPENQTLINSTSEKMKDDLHLLTNAPSIQVD 541
      180  YAK-----GEQSHSLSA-----HLQTLTFGFH-KNDKSPNE----- 213
Db      542  SKKSEGIIGKQKQFACLSRTSCNRSSAGYSTDKNEVEFRGFGARGLKLVNGSEALQAK 601
      214  -----NEQSV-----TLEVLVVCCHKGRDVSQPIRQVTPGKKQVP 251
Db      602  KLFPSDLNINEEYSVEYDRSPSSSKYNDYSMTQIEECNDKNE-----PANKCRL- 652
      252  LIPDLNQTCKGNPPLAVSSNEPEPNSHWKYSLLFR-----VTRPGRRENGM 302
Db      653  -----ILQNNIEMTLDIPEEYTESYRANTENEGNOCTDAGRNTCNSE 695
      303  ING---ETNENIDVNEE---LPARRKKNRDEGKTFYQAQTVVDKRRQLDLDGEV--- 353
      696  SDGSDSKQDVTYIHEENGLPCIDQNDID-----LKLFSQPMKEGNTQIKEGSLDLTC 749
      354  VAAQMEBECPISSKKRATWETILDGKRLPPETP---SOGPTLOFTLRWGTETNDKSTAPLA 411
      750  LVKABETSHVTSNKKOQLTANTGONIKDPDTYLSQTSRKQIKVRSLSLAKASLLN 809
      412  KPLATRN---SSSLHQENKPG-SVKPTQTIAYKESLTTDLQTRKEKDT----- 455
      810  QKWTBEEILNFPDSLNSSELLPGIDIKTD---ISNHEVIENTERKOKITKESLIGTENIL 866
      456  -----PNERQQLRTFYQFLYNNNTRQOTEARDDLHCPCINLCRLYLHLKLSCHS 509
      867  LILQORESKIKIKISAVLGFHTASGKLEITKE-----SLDLVKNLFFBKQDONS 918
      510  RFIENYVYHPKGRIDVSIKCYDG-SYAGNPODIHROPGFARSRNGPVKRTPIYTHILVC 568
      919  E-ITNBSH--RGAKMSQDRBECQDRELACGTTBITTTPEYERTHSLEKQKYSNEIAL 975
      569  RP-----KRT-----KASMSFFLESDGE---VEQRTYSSGHNRL-LYFH 604
      976  RPRLLSDNLKYQTEENLKISDHASQKVVDHENTETETAKKPTMYNQTYSALENSPLTFT 1035
      605  SDPCLPLRPQEMVDSFDE--KQPEMLREKTIQIIEFSD---VNEGEKVMKMLNLYH 658
      1036  QDT---BEKPSVESASLFEAKMKLRE-----GEMDQSERINAAKNCKEYPPDYV 1083
      659  -----MKHGTADNOMNHACMLFVENYGOXTIIKKNLCRN-FMLHLVSMHD---FNLIS 707
      1084  ENPSCGSSNSALTENDKHN---LSBKQSTYLSNSTMNSYSYHGFCHSSEVYVYKSE 1139
      708  IMS-----IDKAVTKLREMO-----QKLEKGESASP 733
      1140  YLSRSKIDNSGIBPVIKNIRERKNIGFSEIMSPGREADTPQSVNDICVEKLATNSCKN 1199
      734  AN-----EETIERQNGTANGFSEINKE-----KALE--TDSVSGVS 768
      1200  KNTAIKVAISDSNNFTIQKLNDSNNSVPAYSTVNSKRVAVAHQTQVTETGFTDNCGMVT 1259
      769  KOSKKOK 775
      1260  KONTYKSK 1266
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RESULT 11
US-09-134-001C-5080
; Sequence 5080, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08

```
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5080  
; LENGTH: 3696  
; TYPE: PRF  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5080
```

Query Match 3.8%; Score 156.5; DB 2; Length 3696;
Best Local Similarity 17.4%; Pred. No. 0.00035; Indels 189; Gaps 32;
Matches 140; Conservative 147; Mismatches 327;

```
QY      30  IEHIEDNHIDTQPRVLEKQELQOPFYVALSYNRFETDAARBOESLKKIOPKLSITLS 89
      1926  LKINNIQOSTQTKNAKQEIYNDKAOEQLQINN--TPDRTBEEKQATNRVAVAGLAQIAQ 1984
      90  SSVSRGNVSTPPRHSGSLTPVTPPTPSSFRSSFTPEPQIYRFLKTRNLADIPLH 149
      1985  -----NINN--AHSQEVNESKTSNIATIKSVQPVVKKPVALNSLTQEAN----- 2028
      150  RUTLTWSHNSKNTIKRK-----TPKVDMLSKYKMGQESHSLAH---LQLTFT 199
      2029  NQKTLIGNDGNATDDEKEAKQLVTQKLEQIQKIHSTQDQVQDVKAQAITAKLI-- 2086
      200  GFPHKNDKPSPNSENEQNSVTLLEVLVVCCHKRQDVSQPIRQVPGKKQVPLIPDLNQT 259
      2087  -----NANAHRQQDAIN---ILTNLAEKSKDIRA--NQDATTEKNTALQSIDT 2132
      260  KQGNFPLAVSSNEPEPNSHWKYSLLFVTRPGRRENGMNG----- 305
      2133  -----LQAAANNINIGANTNALVDENL---EDGKQLORIVLSTQTKTOAKADIAQA 2180
      306  -----ETNENIDVNEELPARRKNRE-----DQEKTFVQGMVFD--KNRRLDLDGE 351
      2181  IGOQRSTIQONQATTEKQKQZALERLQNTNGVNDIQALANQNTDKNNILETIRNV 2240
      352  YEVAQMEBECPISSKKRATWETILDGKRLPPETPSQGPLT---QFTLRWGTETNDKSTA 408
      2241  EPIVIVKPRANELIRKKAQQTLLNQ-----NQDATLEKQIALKLEEVKNKALN 2292
      409  PLAKPLATNSESLSHOEN---KPGSVKPTQITA--VKSLLTTDLQTRKEKQTPNENRQK 462
      2293  QVSO--AHSNNQVKALENNGIAKISEVHPETIIRKNAKQIEBDDQS--QIDTINAN--- 2345
      463  LRIFYQFLNNTNTRQOTEARDDLHCPCWCTLNCRKLYSLKHLKLSRFLFVYVHPKGA 522
      2346  -----NKSTNEKSAID-----RVNAKTIDAI-----NNITNATTT 2377
      523  RIDVSIKCYDGSYAGNPODIHROPGFARSRNGPVKRTPIYTHILVCRPKRTKASMSFLE 582
      2378  QL--VN--DAKNSGNTSISQILPSTA-----VX-----TNALALASBAKNAKNAIIQ 2421
      583  SEDGEVEQORTYSSGHNRLYFHSDTCLPLRPQEMVDSDEKQPEMLREKTIQT----- 637
      2422  TPVATAEKKEKANNKVDRL-----QEBADANILKATTTDEVVNIKN 2462
      638  EERSDVNEBEKEKVMKMLNLYHMKHGTIADNOMNHACMLFVENYGOXTIIKKNLCRNMLH 697
      2463  QAVQNTINAVOVEYIKQONVKQNLQFT--DNQKK-----IIEVTPATLEKKAENANLQ 2516
      698  V-----SMHDFNLISIMSIDKAVTKLREMOQKLEKESASPANETIIEONGTANGF 749
      2517  VLTSTDELTANDVHNNEVQALDKARPKIEIVPVQVSKRDVLAHQEAFNSGTQRIQEN 2576
      750  SEINSEKALELTDVSVGSKQSK 772
      2577  QEATNEKTEALNKINQNLQAK 2599
```

RESULT 12
US-09-710-279-3188
; Sequence 3188, Application US/09710279

Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMELLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/09/710,279
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3188
LENGTH: 1279
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-3188

Query Match 3.8%; Score 153.5; DB 2; Length 1279;
Best Local Similarity 17.5%; Pred. No. 0.00012; Indels 211; Gaps 35;
Matches 141; Conservative 146; Mismatches 310;

30 IEHIEDNHIDTPRVLEKQELQOPTYVALSYINRFMTDARRBOESLKKKIOPKLSLTLS 89
528 LEKINNIOPTQTKNAKQINDKAQEOQLIQINN-TPDATEREKEQATRVAGLAGAQAQ 586
90 SSVSGKGVSTPPRHSGSLTPPVTPPTPSSSFRSSTPEPTQIYRFLTRNLIAPIFLH 149
587 -----NINN--AHSTQEVNESKTSIATIKSVQPVAVIKKPAINSLTQEAN----- 630
150 RFLTYMHSNRSNTIKRK-----TFKVDMLSKVKKMGDESHSLSH-----LQTTT 199
631 NOKTILGNDGNAITDEKEAKQLVTKLNEQIQKHESTQDQVQVNAQAIAITAKLI-- 688
200 GFHHKNDKSPENSEQNSVTLVLVVKVCHKKRQDVSCPIRQVPTKKQVPLIDLNQ 259
689 -----NANAHRQDAIN--ILTNAESKKSDIRA--NODATTEKNAIAISIDT 734
260 KQGNFPSLAVSSNEPEPSNSHWKYSLLFVRTPGRRENGMING----- 305
735 -----LAQAHNNINGANTNALVDENL-----EDGKQLQRIVLSTQTKQAKADIQA 782
306 -----ETNENIDVNEELPARRKRR-----DGEKTFVQAQMYFD-KNRLQLDDE 351
783 IGOORSTIDQNONATTEKEQALERLNOETGNVNRIOALANQVTEKNNILFTIRNV 842
352 YEVAQOEMEBCPISKRAATWETILDGKRLPPETFSQGPL--QFTLRWTGETNDKSTA 408
843 EPIVIVKPRANETIKKAAEQTLTINO-----NODATLEKQIALKLEEVKNAALN 894
409 PIAPLATENSESLHOEN--KPGSVKPTQTLA--VKESLTITDLOTRKEDTPENENROK 462
895 QVSOQ--AHSNNDVKIVENNGIAKISEVHEBTIIEKNAQOIBODQOS-QIDITIAN-- 947
463 LRIFQFLYNNNTROQTEARDLHCPWCTLNCRKLSYLKLKLGHSRTEFVYVHPKA 522
948 -----NKSTNEKSAID-----RVNAKADI-----NNINATTT 979
523 RIDVINECYDGSVYGNPDQIRPOGFAPSRNGPVKRPITHLVCRPKRTAASSEFL 582
980 QV--VN--DAKSGNTSISQILBSTA-----VK--TALAALASEAKKAAIIDQ 1023
583 SEDGEVQORTYSSGHNLVYFHSDFCLPLRQEMEVDSEDEKDPMLREKTTTQI-- 637
1024 TPNAFAEKEKEANNKVDRL-----QEFADANILKATHTDEVANNIKN 1064
638 EEFSSVNBGEKEVMLKMLNHWKGFADNOMNHACMLFVENYQKTIK----- 686
1065 QAVONINAVQVEVIKKQ-----AKNOQLNO-----FIDNQ-KKIIENTPDATLEKA 1110
687 --KNLCRNFMHL--VSMHDFNLISIMSIDKAVTKLRBMQOKLEKGSASPANBEITBE 741

DB 1111 EANRLQVLTSTDSDEIANVNDHNEVDAQLDKARPKAIAIVQVSKKDDALNAIQEAFNS 1170
QY 742 QNGTANGFSEINSEKKALETDSVSGVK 769
DB 1171 QT-----QEIQEKQATNEBKTEALNK 1192

RESULT 13

US-09-248-796A-17551
Sequence 17551, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC.

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17551

LENGTH: 584

TYPE: PRF

ORGANISM: Candida albicans

US-09-248-796A-17551

Query Match 3.7%; Score 151.5; DB 2; Length 584;
Best Local Similarity 19.5%; Pred. No. 5.1e-05;
Matches 129; Conservative 84; Mismatches 201; Indels 249; Gaps 33;

70 RREDSLKKKIOPKLS--LTLSSVSGKGVSTPPRHSGSLTPPVTP-----PITPS 119
61 KGRSEHFNQFQBINNSRPVLLPSSGRDNNNTNIP-----IPILPSSSTNSNNPISS 113
120 SSFRSTTEPTQIYRFLRT-RNLIAPIFLRLTLYMHSRNRNTYKKTFRVDMLSKV 178
114 SNSRWFSPNVPVPLPVVTPPSSALSPPTQI-----HQOQOQDLHK-FRTSNGSNT 165
179 EKKMGEGSHSLSAHL-----QLTGPFHKNDKSPENSEQNSVTLVLVVKCHKKRK 234
166 PITGGIGSSPTSTILANSANISY-----RSQPLKDNQOTSSTK----- 206
235 DVSCPIRQVPTKKQVPLIPDLNQTGKGNFSLAVSNE--PEPSNSHWKYSLLFR 290
207 -----DNNNT-----IENEDQKFLAKEBALV----- 229
291 VTRPGRREFNNGINEN--IDVNEELPARRKRRNEDGKTFVQAQMYFDKRRQLQ 347
230 ATAKGVKTNHNNNGKFGNNTSKIDINNH--NKNNNNSDNET-ILDSTIADLRLLOY 286
348 LDGEYEVAMOEMEBCPISKRAATWETILDGKRLPPETFSQGPLQ--FTLRWTGETND 404
287 ASAPHGNPIGQISGLQNTSKEL-----LEVQDYVSNPDDLQNNNFRKANNGDNN 336
405 KSTAPIAKPLATRNSESLHOE--NKPQ-----SVKPTQ-----TIA 438
337 TTS-----NSKSNVNHHPSGNBPNNFLDEASTTTSNNTNRSTGTGTGIGATTNI 389
439 VKESLTITDLOTRKED-----TPENRQQLRIFQFLYNNNTROQTEAD- 483
330 ISES--ESBLKVKRBSIANIINPSTTTTSTTNN-----NNNTSSSTKTKY 436
484 -----DLHCPWCTLNCRKLSYLKLKLGHSRTEFVYVHPKARIDVINECYDGSYA 537
437 SODPRTKRPCKCKMSPFRSSDLKHK-----OHL 467
538 GNPDQIRPOGFAPSRNGPVKRPITHI--LVCRPKRTKASMEFL-----E 582
468 TTPNLCQFCGKGFARQALKR-----HIGTLTCKRNDKCKLYENTLVNLSQODDDAE 523

TELEPHONE: 207-363-0558
TELEFAX: 207-363-0528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 912 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-005-002C-8

Query Match 3.7%; Score 150; DB 1; Length 912;
Best Local Similarity 18.5%; Pred. No. 0.00015;
Matches 153; Conservative 126; Mismatches 287; Indels 260; Gaps 37;

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OY MTDARREOESLKKLIQPLSLTLSSVSGNVSTPPRSSGLTPPYTPPTSSSPRS 124
DB 3 MODAKESYSMPK-----TSSPPPTPTNQIPYQADPLQMGYIQ 45
OY 125 STPEPTQI--YRPLRTNLI--APIPLHRT-----LYMSHRN-----SRTNIRKRTF 169
DB 46 APYLYPTQIPAYSF---NMVNQNPYI-HQSGSPHLRPQNNINGSTNNNNINKKKW 100
OY 170 KYDDMLSKVEKKKGQESHSLSAHLQLTFGFFHKDK-----PSPNS-----E 213
DB 101 HSNGITNN-NGSSGNQANSSGSGMSYNSKHTYHNYSNNHI PMMASPSNGSNAQMKQT 159
OY 214 NEQN-----SVTLEVLVYVCHKRRKDVSCPIRQVPTGKKQVPLIPDLNQ 259
DB 160 NSSNGNSSATSPSYSSYSSSQDYLYKFDVTKLV---LKSSNLIQLPLF--INTT 213
OY 260 KFG-----NPSLAVSSNEPEPSN-----SHVKSYSLLFVTRPREPFNGM 302
DB 214 EAEFAAGYQRYELMMKALNINSESLSSVEKSAHHHTKSHI-----PKHNE 264
OY 303 INGETN-ENIDVNEELPARKKRNREDGKTFVAQMTVPDKNRLLQLDGEYEVANQEMEE 361
DB 265 VKTEHGEEDAHDKKPHASKDAHELKCKTEYVK-----EDAKQDRNE 307
OY 362 CPISKRTATWETILDGKLPPEPTFSQGPFTLOFTLRMTGETNDKSTAPIA---KPLATR 417
DB 308 KYIQEPQATVLFVYVKKK--PEESVEEN-----TSKTSPPSPSPAASATIASD 356
OY 418 NSESLHQRKPGSVKPTQTIAYKESLITTDLQTRKEKQTPENENRQKLIFYOFLYNNNTRO 477
DB 357 AIKSKQANRKTYSVSGSMVTKTPISGTTAGVSSNNMAATIGKSSPL-----LSK 405
OY 478 QTEARDDLHCWCTLNCRKLYSLKHLKLSRFTFNVTYHPKARIDVINSINECYDSYA 537
DB 406 QPKDKKTYVPSTKGIIEPLGSA--LRMCEPDPIISYLRNKDVENKIPVHSII----- 458
OY 538 GNPQDIHQPGAFSRNGPVKRTPIITHLVCRP-----KRTYASM----- 577
DB 459 --PRGIINRANICF-----MSSVLQVLLYCKPPIDIVINVLSTRNTNSRVGTSSCKLLDA 510
OY 578 -----SEPLESEDG--EVEQARTYSSGHRNLYPHSDTCLPLRQEMEVADSE 621
DB 511 CLTWYKQPKDEYKFKFLFNADDAKTESDAKSKSKSPQHCATADAVKDEP----- 565
OY 622 DEKQDEMLREKTTIOIEEPSDVNBEKEVKMLNLVYMKH-----GFIADNQNMHA 672
DB 566 -----YKLSITIPKFKDLQWGHDAEFLTHLDQLHEELISAIDGLTNE----- 612
OY 673 CMLFVENYGGKIKKNLCRNFELHVSMM--DENVLISIMSIDKAVTKLRQMOQLKEGE 729
DB 613 ---IQNNMQSINDQQL--KVFPIRNLRSYGKAEF-----IKNASPRIKELEIKY----- 656
OY 730 SASPANBEITEONGTANGFSEINSKERALEFTDSVSGVSKOSKKOK 775
DB 657 --GVINDSTEE-----NGMHE-----VSGSSKKGKXTK 683
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Job time : 52 secs

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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:17:23 ; Search time 170 Seconds
(without alignments)
1907.268 Million cell updates/sec

Title: US-09-874-162a-8
Perfect score: 4078
Sequence: 1 MTGIAAASFNTCRFGCGG.....KALETDSVSGVSKQKQKL 776

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4078	100.0	776	3	US-09-874-162a-8 Sequence 8, Appli
2	3413	83.7	739	3	US-09-874-162a-5 Sequence 5, Appli
3	3413	83.7	803	3	US-10-942-711-16 Sequence 16, Appl
4	2043	47.1	388	3	US-09-764-864-931 Sequence 931, App
5	1944	47.7	367	5	US-10-942-711-54 Sequence 54, Appl
6	1497	36.7	289	3	US-09-764-864-911 Sequence 911, App
7	1453	33.6	292	3	US-09-764-864-1369 Sequence 1369, Ap
8	1127.5	27.6	955	6	US-11-097-143-41697 Sequence 41697, A
9	919	22.5	175	3	US-09-764-864-1355 Sequence 1355, Ap
10	661	16.2	243	3	US-09-874-162a-2 Sequence 2, Appli
11	661	16.2	243	4	US-10-144-198-16 Sequence 16, Appl
12	661	16.2	243	4	US-10-104-047-2404 Sequence 2404, Ap
13	652	16.0	278	3	US-09-764-864-1334 Sequence 1334, Ap
14	476	11.7	143	3	US-09-764-864-884 Sequence 884, App
15	359	8.8	69	4	US-10-029-386-28495 Sequence 28495, A
16	280	6.9	171	4	US-10-276-774-2060 Sequence 2060, Ap
17	236	5.8	735	4	US-10-425-115-276256 Sequence 6320, Ap
18	226.5	5.6	626	5	US-10-739-930-6320 Sequence 6320, Ap
19	224	5.5	767	6	US-11-097-143-1512 Sequence 1512, Ap
20	221	5.4	440	5	US-10-739-930-6330 Sequence 6330, Ap
21	221	5.4	445	5	US-10-942-711-2 Sequence 2, Appli
22	217	5.3	440	5	US-10-942-711-5 Sequence 5, Appli
23	214.5	5.3	813	4	US-10-231-778-2 Sequence 2, Appli
24	211	5.2	692	4	US-10-177-478-6 Sequence 6, Appli
25	210.5	5.2	481	4	US-10-425-114-54921 Sequence 54921, A
26	205.5	5.0	640	4	US-10-437-963-193525 Sequence 193525, A
27	199.5	4.9	435	4	US-10-425-114-46823 Sequence 46823, A

28	195	4.8	635	4	US-10-425-115-256141 Sequence 256141,
29	192.5	4.7	428	4	US-10-424-599-254264 Sequence 254264,
30	184.5	4.5	598	4	US-10-425-115-276234 Sequence 276234,
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32	176.5	4.3	1142	4	US-10-369-493-1700 Sequence 1700, Ap
33	176.5	4.3	1142	4	US-10-618-581-10 Sequence 10, Appl
34	175	4.2	1349	4	US-10-732-923-2883 Sequence 2883, Ap
35	170.5	4.2	1396	5	US-10-732-923-2883 Sequence 412, App
36	161.5	4.0	583	4	US-10-451-467A-412 Sequence 5942, Ap
37	156.5	3.8	3696	4	US-10-724-972A-5942 Sequence 1345, Ap
38	155.5	3.8	1328	4	US-10-083-357-1345 Sequence 71235, A
39	153.5	3.8	3692	4	US-10-282-122A-71235 Sequence 1332, Ap
40	152	3.7	1322	4	US-10-083-357-1332 Sequence 2070, Ap
41	152	3.7	1957	4	US-10-369-493-2070 Sequence 3328, Ap
42	152	3.7	1957	5	US-10-732-923-3328 Sequence 7646, Ap
43	151	3.7	1881	4	US-10-032-585-7646 Sequence 1772, Ap
44	150	3.7	912	4	US-10-369-493-1772 Sequence 3329, Ap
45	149.5	3.7	1015	5	US-10-732-923-3329

ALIGNMENTS

RESULT 1									
US-09-874-162a-8									
; Sequence 8, Application US/09874162A									
; Patent No. US20020155452A1									
; GENERAL INFORMATION:									
; APPLICANT: Koonitz, Jaeson									
; TITLE OF INVENTION: FUSION OF JAZF1 AND JAZA1 GENES IN									
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS									
; FILE REFERENCE: 05311-024001									
; CURRENT APPLICATION NUMBER: US/09/874,162A									
; PRIOR FILING DATE: 2001-06-04									
; PRIOR APPLICATION NUMBER: US 60/209,093									
; NUMBER OF SEQ ID NOS: 23									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 8									
; LENGTH: 776									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
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Best Local Similarity 100.0%; Score 4078; DB 3; Length 776;									
Best Local Similarity 100.0%; Pred. No. 7.3e-309;									
Matches 776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MTGIAAASFNTCRFGCGGHPPTLADLIEHIEDNHTDTPRVLEKELQOPTVALSY	60						
DB	1	MTGIAAASFNTCRFGCGGHPPTLADLIEHIEDNHTDTPRVLEKELQOPTVALSY	60						
QY	61	INRFMTDAREBOESLKKKIQPKLSTLSSSVSRGNVSTPPRHSGSLTPPTPTPSS	120						
DB	61	INRFMTDAREBOESLKKKIQPKLSTLSSSVSRGNVSTPPRHSGSLTPPTPTPSS	120						
QY	121	SFRSSTPEPQIYRFLTRNLAPIFLHRLTYSHNSKRTNIRKTKFYKDDMLSKYEK	180						
DB	121	SFRSSTPEPQIYRFLTRNLAPIFLHRLTYSHNSKRTNIRKTKFYKDDMLSKYEK	180						
QY	181	MKGEOESLSLAHQLTFTGFPHNDKSPNSEKONSVTLEVLVKKCHKKRXOVSCPI	240						
DB	181	MKGEOESLSLAHQLTFTGFPHNDKSPNSEKONSVTLEVLVKKCHKKRXOVSCPI	240						
QY	241	ROVPTGKKQVPLIDNLQTKGPNPPLAVSSNEPEPSNHWKYSLLFRYTRPGRRFN	300						
DB	241	ROVPTGKKQVPLIDNLQTKGPNPPLAVSSNEPEPSNHWKYSLLFRYTRPGRRFN	300						
QY	301	GMINGETMENTDNVEELPARKKRNREDEKTFVAMTYFDKRRQLQLDGSEYVAMQME	360						
DB	301	GMINGETMENTDNVEELPARKKRNREDEKTFVAMTYFDKRRQLQLDGSEYVAMQME	360						

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Qy 361 ECPISKKRATWETIILDKGLPPETFSQGPPTLOFTLRMTGETNDKSTAPIAKPLATRNSE 420
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Qy 421 SLHQENKPGSVKPTQTTIAVESITTDLOTRKEKOTPNENOKLRIFYOPLYNNTROOTE 480
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Db 421 SLHQENKPGSVKPTQTTIAVESITTDLOTRKEKOTPNENOKLRIFYOPLYNNTROOTE 480
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Qy 481 ARPDLCPCWCTLNCRKLYSLKHLKICHSRPFINYYVHPGARIIDVINCDCGYAGNPD 540
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Db 481 ARPDLCPCWCTLNCRKLYSLKHLKICHSRPFINYYVHPGARIIDVINCDCGYAGNPD 540
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Qy 541 QDIHRPGFAPSNNGVVKRTPIITHILVCRPKRTKASNEFLSEDEGEVQORTYSSGHR 600
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Qy 601 LYHSTQCLPLRQEBEVDSEKDPMLREKTTTQIEEESDVNEGEKEVMKLMNLMHVK 660
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Db 661 HGFIADNOMNHCMLFVENYGOKIIRKNCRNFMHLVSMHDFNLISIMSIDKAVTKLRE 720
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Qy 721 MOCKLEKGSASPANEIITEBONGTANGFSEINSKEKALETDSVSGVSKOKKL 776
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Db 721 MOCKLEKGSASPANEIITEBONGTANGFSEINSKEKALETDSVSGVSKOKKL 776
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RESULT 2
US-09-874-162a-5
; Sequence 5, Application US/09874162a
; Patent No. US20020155452a1
; GENERAL INFORMATION:
; APPLICANT: Koonitz, Jason
; APPLICANT: Sklar, Jeffrey
; TITLE OF INVENTION: FUSION OF JAZZ1 AND JAZZ2 GENES IN
; FILE REFERENCE: 05311-024001
; CURRENT APPLICATION NUMBER: US/09/874, 162a
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209, 093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-162a-5
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Best Local Similarity 99.8%; Pred. No. 5.1e-257;
Matches 647; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 129 EPTQIRFLATRNILAPIFLHRTLTYMSHRNSRTNIKRTFKYDDMLSKYKKKGEQESH 188
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Db 92 KPTQIRFLATRNILAPIFLHRTLTYMSHRNSRTNIKRTFKYDDMLSKYKKKGEQESH 151
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Qy 189 SLSAHLQTLFTGFFHNKDKSPNSNEQNSVTLLEVLVVCYCHKRQDVSCPIRQVPTGKK 248
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Db 152 SLSAHLQTLFTGFFHNKDKSPNSNEQNSVTLLEVLVVCYCHKRQDVSCPIRQVPTGKK 211
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Qy 249 QVPLIDNLNQTGKGNPSSLAVSNEPEPSNSHWKYSISLLFRVTRPGRREFGNMGENTN 308
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Db 212 QVPLIDNLNQTGKGNPSSLAVSNEPEPSNSHWKYSISLLFRVTRPGRREFGNMGENTN 271
|
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Qy 309 ENIDVNEELPARRKRNREDGEKTFVAQMTVPDKNRRLQLLDGEYEVAMQEMECPSISKR 368
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Db 272 ENIDVNEELPARRKRNREDGEKTFVAQMTVPDKNRRLQLLDGEYEVAMQEMECPSISKR 331
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Qy 369 ATWETIILDKRLPPETFSQGPPTLOFTLRMTGETNDKSTAPIAKPLATRNSESLHQENK 428
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Db 332 ATWETIILDKRLPPETFSQGPPTLOFTLRMTGETNDKSTAPIAKPLATRNSESLHQENK 391
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|
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Db 392 GSVKPTQTTIAVESITTDLOTRKEKOTPNENOKLRIFYOPLYNNTROOTEARDLHCP 451
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|
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Qy 489 WCTLNCRKLYSLKHLKICHSRPFINYYVHPGARIIDVINCDCGYAGNPDQIHRQPG 548
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|
|
Db 452 WCTLNCRKLYSLKHLKICHSRPFINYYVHPGARIIDVINCDCGYAGNPDQIHRQPG 511
|
|
|
Qy 549 PAFSRNGPKRTPIITHILVCRPKRTKASNEFLSEDEGEVQORTYSSGHRNLYPHSDTC 608
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Db 512 PAFSRNGPKRTPIITHILVCRPKRTKASNEFLSEDEGEVQORTYSSGHRNLYPHSDTC 571
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Qy 609 LPLRQEBEVDSEKDPMLREKTTTQIEEESDVNEGEKEVMKLMNLMHKGFIADNQ 668
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|
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Db 572 LPLRQEBEVDSEKDPMLREKTTTQIEEESDVNEGEKEVMKLMNLMHKGFIADNQ 631
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Qy 729 ESASPANEIITEBONGTANGFSEINSKEKALETDSVSGVSKOKKL 776
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RESULT 3
US-10-942-711-16
; Sequence 16, Application US/10942711
; Publication No. US20050132446a1
; GENERAL INFORMATION:
; APPLICANT: Dean, Caroline
; APPLICANT: Gendall, Anthony
; TITLE OF INVENTION: Methods and means for modification of plant characteristics using
; FILE REFERENCE: Mewburn
; CURRENT APPLICATION NUMBER: US/10/942, 711
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US/09/890, 220
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/GB00/00248
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: GB 9901927.5
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-942-711-16
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Query Match      83.7%; Score 3413; DB 5; Length 803;
Best Local Similarity 99.8%; Pred. No. 5.8e-257;
Matches 647; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 129 EPTQIRFLATRNILAPIFLHRTLTYMSHRNSRTNIKRTFKYDDMLSKYKKKGEQESH 188
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Db 156 KPTQIRFLATRNILAPIFLHRTLTYMSHRNSRTNIKRTFKYDDMLSKYKKKGEQESH 215
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|
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Qy 189 SLSAHLQTLFTGFFHNKDKSPNSNEQNSVTLLEVLVVCYCHKRQDVSCPIRQVPTGKK 248
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Db 216 SLSAHLQTLFTGFFHNKDKSPNSNEQNSVTLLEVLVVCYCHKRQDVSCPIRQVPTGKK 275
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Qy 249 QVPLIDNLNQTGKGNPSSLAVSNEPEPSNSHWKYSISLLFRVTRPGRREFGNMGENTN 308
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Db 276 QVPLIDNLNQTGKGNPSSLAVSNEPEPSNSHWKYSISLLFRVTRPGRREFGNMGENTN 335
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Qy 309 ENIDVNEELPARRKRNREDGEKTFVAQMTVPDKNRRLQLLDGEYEVAMQEMECPSISKR 368
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Db 336 ENIDVNEELPARRKRNREDGEKTFVAQMTVPDKNRRLQLLDGEYEVAMQEMECPSISKR 395
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Qy 369 ATWETLLDGRRLPPEFTPSGPTLQTLNWTGETNDKSTAPIAKPLATNSESJLHQNKP 428
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Db 396 ATWETLLDGRRLPPEFTPSGPTLQTLNWTGETNDKSTAPIAKPLATNSESJLHQNKP 455
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Db 456 GSVKPTQTIAVKSLLTTDQTRKEKTPPENRQKLI FYQFLYNNNTRQOTEARDLHCP 515
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Db 516 WCTLNCRKLYSLKLHLKLGSRPIFYVYVHPKARIDVSNCEYDGSYAGNPODIHROP 575
Qy 549 FAFSRNGPVKRTPTIHLVCRPKRTASMSSEFLSEDEGEVQORTYSSGHNLRYFHSDFC 608
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Db 576 FAFSRNGPVKRTPTIHLVCRPKRTASMSSEFLSEDEGEVQORTYSSGHNLRYFHSDFC 635
Qy 609 LPLRPOEMEVDSDEDEKDEPMLRKTTTQIBESDVNVEGEVWKLNNLHVMMKGFADNQ 668
|
Db 636 LPLRPOEMEVDSDEDEKDEPMLRKTTTQIBESDVNVEGEVWKLNNLHVMMKGFADNQ 695
Qy 669 MNHACMLFVENYGOKIILKKNLCBNFMLHVSMDPFLISMSIDKAVTKLREMOQKLEKG 728
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Qy 729 ESASPANBEITEBQNTANGFSEINSKERALETDSVSGVSKOKKOKL 776
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RESULT 4
US-09-764-864-931
; Sequence 931, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 931
; LENGTH: 388
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-764-864-931
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Query Match 50.1%; Score 2043; DB 3; Length 388;
Best Local Similarity 99.5%; Pred. No. 1.5e-150;
Matches 386; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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|
Db 121 SHFIFNYVYHPKARIDVSNCEYDGSYAGNPODIHROPFAFSRNGPVKRTPTIHLVYC 180
Qy 569 RPKRTKASMSSEFLSEDEGEVQORTYSSGHNLRYFHSDFCPLRPOEMEVDSDEKDEP 628
|
Db 181 RPKRTKASMSSEFLSEDEGEVQORTYSSGHNLRYFHSDFCPLRPOEMEVDSDEKDEP 240
Qy 629 LREKTTTQIBESDVNVEGEVWKLNNLHVMMKGFADNQMNHACMLFVENYGOKIILKKN 688
|
Db 241 LREKTTTQIBESDVNVEGEVWKLNNLHVMMKGFADNQMNHACMLFVENYGOKIILKKN 300
Qy 689 LCRNFMHLVSMHDFLISMSIDKAVTKLREMOQKLEKGSASPANBEITEBQNTANG 748
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Db 301 LCRNFMHLVSMHDFLISMSIDKAVTKLREMOQKLEKGSASPANBEITEBQNTANG 360
Qy 749 FSEINSKERALETDSVSGVSKOKKOKL 776
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Db 361 FSEINSKERALETDSVSGVSKOKKOKL 388
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RESULT 5
US-10-942-711-54
; Sequence 54, Application US/10942711
; Patent No. US20050132446A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Caroline
; APPLICANT: Gendall, Anthony
; TITLE OF INVENTION: Methods and means for modification of plant characteristics us1
; FILE REFERENCE: Mewburn
; CURRENT APPLICATION NUMBER: US/10/942,711
; PRIOR FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US/09/890,220
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/GB00/00248
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: GB 9901927.5
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 54
; LENGTH: 367
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-942-711-54
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Best Local Similarity 100.0%; Pred. No. 7.2e-143;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 181 QORTYSSGHNLRYFHSDFCPLRPOEMEVDSDEKDEPMLRKTTTQIBESDVNVEGEK 240
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Db 301 SIDKAVTKLREMOQKLEKGSASPANBEITEBQNTANGFSEINSKERALETDSVSGVSK 360
Qy 770 QSKKOKL 776
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Db 361 QSKKOKL 367
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RESULT 6
US-09-764-864-911
; Sequence 911, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 911
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-864-911

Query Match
Best Local Similarity 36.7%; Score 1497; DB 3; Length 289;
Matches 283; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 6 DCRKLYSLKHLKLCRSRIFNYVYHPKGRIDVSNCEYDGSYAGNPQDIHQPGPAFS 65
QY 553 RRGVRRPTTHLVNCRPKTKASMSSEFLSEDEGEVQOQTYSSGHNRLYFHSDTCLPIR 612
;
DB 66 RRGVRRPTTHLVNCRPKTKASMSSEFLSEDEGEVQOQTYSSGHNRLYFHSDTCLPIR 125
QY 613 PQMEVDSDEKDPKPEMLREKTIQIEFSDVNGEKEVMKMLNLYMKHGFIDNOMNHA 672
;
DB 126 PQMEVDSDEKDPKPEMLREKTIQIEFSDVNGEKEVMKMLNLYMKHGFIDNOMNHA 185
QY 673 CMLFVENVGQKIKKIKNLCRNFMHLVSMHDFNLISIMSDIKAVTKLREMOQKLEKESAS 732
;
DB 186 CMLFVENVGQKIKKIKNLCRNFMHLVSMHDFNLISIMSDIKAVTKLREMOQKLEKESAS 245
QY 733 PANEETEEONGTANGPSEIENSKKALETDSVGSVSKOSKQKL 776
;
DB 246 PANEETEEONGTANGPSEIENSKKALETDSVGSVSKOSKQKL 289

RESULT 7
US-09-764-864-1369
; Sequence 1369, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1369
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (121)
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-864-1369

Query Match
Best Local Similarity 35.6%; Score 1453; DB 3; Length 292;
Matches 275; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 233 RKDVSCPIQVPTGKQKQVLIPLDNLQTKRGNPPLAVSSNEFPSPSHVYKSYSLFRYT 292
;
DB 1 KDVSCPIQVPTGKQKQVLIPLDNLQTKRGNPPLAVSSNEFPSPSHVYKSYSLFRYT 60
QY 293 RGRREFFNGMNGENTENIDVNEELPARKRRREDEKTFVQOMTFDQNRRLQLDGXY 352
;
DB 61 RGRREFFNGMNGENTENIDVNEELPARKRRREDEKTFVQOMTFDQNRRLQLDGXY 120
QY 353 EVAMQEMECPISKKRAWTETILDGKRLPPFTFSGPTLOFTLAWTGETNDKSTAPIAK 412
;
DB 121 XVAQMEMECPISKKRAWTETILDGKRLPPFTFSGPTLOFTLAWTGETNDKSTAPIAK 180
QY 413 PLATNRSSELIQBNKPGSVKPTQITAVKESLTTDLOTREKQTPNENRQKALIFYQFLYN 472
;
DB 181 PLATNRSSELIQBNKPGSVKPTQITAVKESLTTDLOTREKQTPNENRQKALIFYQFLYN 240
QY 473 NNTROQTEARDDLHCPWCTLNCRKLYSLKHLKLCRSRIFNYV 516
;
DB 241 NNTROQTEARDDLHCPWCTLNCRKLYSLKHLKLCRSRIFNYV 284

RESULT 8
US-11-097-143-41697
; Sequence 41697, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41697
; LENGTH: 955
; TYPE: PRT
; ORGANISM: DROSOPHILA
; US-11-097-143-41697

Query Match
Best Local Similarity 27.6%; Score 1127.5; DB 6; Length 955;
Matches 273; Conservative 17; Mismatches 240; Indels 179; Gaps 26;

QY 65 MTDARREDSLKKKIQPLSLTLSSSVSRGNV---STPPRHSGSLTPPVTPITPPSS 120
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```

Db      1  MAPAKKREKDS-----NPDGSANGIIIGLTHGAPDASNNGSTVPTAEQGVKLN 49
Qy      121 SFRSSTP-----TEPTQYRFLRTRNLAPIFLRLTLTYMHRSRTYKAKTKVDNM 174
Db      50 GHQBOEQLFLOAFEEPTQYRFLRNRHETNP1FLNRKTSYMEKERSRNKKRISFQVNSM 109
Qy      175 LSKVEKMKGEQESHSLSA-HLQTLFGFPHKNDKXSPNSENQ-----NSVYLE 222
Db      110 LEST-----TQKSEAVSQNYLHVITYDSLHEKLPARLDNDSGDDLQEOQLCEAGSSVSTE 164
Qy      223 VLVAVCHKKRQDVSCPIRQVPTGKKQVPLIPDLNQTCKGNPPSLAVSSNEEP-SNSHM 281
Db      165 TLVYKTRSKRQDSTLDFQELLSKCSQIYYNP--KDRYGHATISIPLOQTRPMGEQHT 221
Qy      232 VKSYSLLRVYTRPRGRREFGNGMNGETNEIDVNEELPARKKNREDDEKTFVACMTVPK 341
Db      222 L--YKLLPRIK-----VLSPSTCN--DENAEPTP-NKRSRPN-EKMFQSESLIYEX 266
Qy      342 NRRLQLDGEYEVAMQEMECPI---SKKRAWTETILDGKRLP---PFETFSQGPLQPT 395
Db      267 SSGF-ITGEYRAMLOPLANSTISKSPKCKTWEIWD-SYPLSLITVDVYQSPMLKFN 324
Qy      336 LRMGTETNDKSTAPIAKPLATE-----NSESIAQEN-----KPGSVKPTQTI 437
Db      325 LTL--SNEQLPEMISAPELQRYVQHLDAVAMNMYNNNNNNNCSGLKNGSGGNGSTV 381
Qy      438 AVKESLTLDLQTRKCKQTPNENRQKRLFYQPLYYNNTRQOETEAADDLHCPECTLANCKL 497
Db      382 C-----KTPP---EHIQIYVNFMYNSNNTROQTEYQELNCPWCGLDCLRL 423
Qy      498 YSLKHLKLCHSRFIFNYVYHFKGARIDVSYNECYDGSYAGNODIHPGPAFSRN-GP 556
Db      424 YALLKHLKLCARFETQTPAGSGAKRIDVTIINDAYDSYAGSPYDLAPSGSSFPKRTGCP 483
Qy      557 VKRPIITHLVCRPRRTASMSSEPLESBDEVEBOQRTYSSGNRLRYFHSDTCLPLRPOEM 616
Db      484 VRTSVTSLMVCRRPQKCTCLDEFLDEDEISNRSYITGNRLRYHHTETCLPLVPHREL 543
Qy      617 EVDSDDEQPEWLEKTKTTOIIEESDVNVEGEKVCNKLNLHYMKGFADNOMNACHMLF 676
Db      544 DIDSSESDBPLMRKTKTOMTDEFSDVNBGEKELMKNLNLHYMRGFGVDCOLPLACMF 603
Qy      677 VENYGOKIIRKQICENFMHLVSMHDFNLISMSIDKAVTKLREMOQKLEKES----- 730
Db      604 LPAKTEIVRKQLYNFIHMCSLPDYGLIAETVYKTVQKLQGLSKYAMAGQELMQROR 663
Qy      731 -----ASPANBEITE----- 740
Db      664 EEOUKYWLVDGWHKKQEDPKTLKSPQKRAPRADQASTSSASGSSGSSSMQPKMPA 723
Qy      741 -----EONGTANGFSEINSEKALETDSVSGVSKQSKQKYL 776
Db      724 HLKRGSAASSPGVQKGTENGNGSNS-----SSSNSKQVAKKSDQPL 767

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RESULT 9

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US-09-764-864-1355
; Sequence 1355, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; PTL REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1355
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (166)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1355

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Query Match      22.5%; Score 919; DB 3; Length 175;
Best Local Similarity 94.3%; Pred. No. 2.2e-63;
Matches 165; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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```

Qy      466 FYQPLNNNTROQTEARDLHCPWCTLNCRLKLSLKLKLCCHSRFINVYVHPKGARID 525
Db      1 FYQPLNNNTROQTEARDLHCPWCTLNCRLKLSLKLKLCCHSRFINVYVHPKGARID 60
Qy      526 VSINECYDGSYAGNPQDIHRQPGAFSRNGVYKRTPIHIIIVCRPKRTKASMSSEPLESBD 585
Db      61 VSINECYDGSYAGNPQDIHRQPGAFSRNGVYKRTPIHIIIVCRPKRTKASMSSEPLESBD 120
Qy      586 GEVEQORTYSSGNRLRYFHSDTCLPLRPOEMVDSDEKDEPWLREKTTIOIEBF 640
Db      121 GEVEQORTYSSGNRLRYFHSDTCLPLRPOEMVDSDEKDEPWLREKTTIOIEBF 175

```

RESULT 10

US-09-874-162a-2

```

; Sequence 2, Application US/09874162A
; Patent No. US20020155452A1
; GENERAL INFORMATION:
; APPLICANT: Koonitz, Jason
; APPLICANT: Sklar, Jeffrey
; TITLE OF INVENTION: FUSION OF JAZF1 AND JAZ2 GENES IN
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
; FILE REFERENCE: 05311-024001
; CURRENT APPLICATION NUMBER: US/09/874,162A
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-162a-2

```

```

Query Match      16.2%; Score 661; DB 3; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MTGIAAASFPSNTCRFGCGGHPPTLADLIEHIDNHIDTPRYLKEQELQOPTYVALSY 60
Db      1 MTGIAAASFPSNTCRFGCGGHPPTLADLIEHIDNHIDTPRYLKEQELQOPTYVALSY 60
Qy      61 INREMTDAARREQSLKKKIQPKLSLTLSVSVSRGNVSTPRRHSGSLTPVTPPTPSS 120
Db      61 INREMTDAARREQSLKKKIQPKLSLTLSVSVSRGNVSTPRRHSGSLTPVTPPTPSS 120
Qy      121 SFRSSTP 128
Db      121 SFRSSTP 128

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RESULT 11

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US-10-144-198-16
; Sequence 16, Application US/10144198
; Publication No. US20030219748A1
; GENERAL INFORMATION:

```

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/ APPLICANT: Origene Technologies Inc
/ TITLE OF INVENTION: Regulated Prostate Cancer Genes
/ FILE REFERENCE: 9U 105 R1
/ CURRENT APPLICATION NUMBER: US/10/144,198
/ CURRENT FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 16
/ LENGTH: 243
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-144-198-16

Query Match      16.2%; Score 661; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGIAASFPSNTRCFGGCGLHPTLADLIEHIEDNHIDTDPVLEKQELQOPTVVALSY 60
DB 1 MTGIAASFPSNTRCFGGCGLHPTLADLIEHIEDNHIDTDPVLEKQELQOPTVVALSY 60
QY 61 INRFMTDAARREOESLKKKIOPKLSLTLSSSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120
DB 61 INRFMTDAARREOESLKKKIOPKLSLTLSSSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120
QY 121 SFRSSTPT 128
DB 121 SFRSSTPT 128

RESULT 12
US-10-104-047-2404
/ Sequence 2404, Application US/10104047
/ Publication No. US20030236392A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. US20030236392A1el full length cDNA
/ FILE REFERENCE: H1-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 2404
/ LENGTH: 243
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-104-047-2404

Query Match      16.2%; Score 661; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGIAASFPSNTRCFGGCGLHPTLADLIEHIEDNHIDTDPVLEKQELQOPTVVALSY 60
DB 1 MTGIAASFPSNTRCFGGCGLHPTLADLIEHIEDNHIDTDPVLEKQELQOPTVVALSY 60
QY 61 INRFMTDAARREOESLKKKIOPKLSLTLSSSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120
DB 61 INRFMTDAARREOESLKKKIOPKLSLTLSSSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120
QY 121 SFRSSTPT 128
DB 121 SFRSSTPT 128

RESULT 13
US-09-764-864-1334
/ Sequence 1334, Application US/09764864
/ Patent No. US20020132753A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
```

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/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT223
/ CURRENT APPLICATION NUMBER: US/09/764,864
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 1792
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1334
/ LENGTH: 278
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (145)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1334

Query Match      16.0%; Score 652; DB 3; Length 278;
Best Local Similarity 99.2%; Pred. No. 2.9e-42;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTGIAASFPSNTRCFGGCGLHPTLADLIEHIEDNHIDTDPVLEKQELQOPTVVALSY 60
DB 36 MTGIAASFPSNTRCFGGCGLHPTLADLIEHIEDNHIDTDPVLEKQELQOPTVVALSY 95
QY 61 INRFMTDAARREOESLKKKIOPKLSLTLSSSVSRGNVSTPPRHSSGSLTPPTPTPPSS 120
DB 96 INRFMTDAARREOESLKKKIOPKLSLTLSSSVSRGNVSTPPRHSSGSLTPPTPTPPSS 155
QY 121 SFRSSTPT 128
DB 156 SFRSSTPT 163

RESULT 14
US-09-764-864-884
/ Sequence 884, Application US/09764864
/ Patent No. US20020132753A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT223
/ CURRENT APPLICATION NUMBER: US/09/764,864
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 1792
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 884
/ LENGTH: 143
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-764-864-884

Query Match      11.7%; Score 476; DB 3; Length 143;
Best Local Similarity 100.0%; Pred. No. 6e-29;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGIAASFPSNTRCFGGCGLHPTLADLIEHIEDNHIDTDPVLEKQELQOPTVVALSY 60
DB 51 MTGIAASFPSNTRCFGGCGLHPTLADLIEHIEDNHIDTDPVLEKQELQOPTVVALSY 110
QY 61 INRFMTDAARREOESLKKKIOPKLSLTLSSSVS 93
DB 111 INRFMTDAARREOESLKKKIOPKLSLTLSSSVS 143

RESULT 15
US-10-029-386-28495
/ Sequence 28495, Application US/10029386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rosen et al.
```



```
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28495
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR17.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: P23477, EVALUE 2.70e+00
US-10-029-386-28495
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Query Match      8.8%; Score 359; DB 4; Length 69;
Best Local Similarity 98.6%; Pred. No. 2.7e-20;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 569 RPKRTKASMSSEFLSGDGEVEEOQRTYSSGHNRLYFHSDTCLPLRPOEMEVDSDEKDPW 628
DB 1 RPKRTKASMSSEFLSGDGEVEEOQRTYSSGHNRLYFHSDTCLPLRPOEMEVDSDEKDPW 60
QY 629 LREKTTTQI 637
DB 61 LREKTTTIV 69
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Job time : 172 secs

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 7, 2006, 13:18:27 ; Search time 28 Seconds
(without alignments)
864.464 Million cell updates/sec

Title: US-09-874-162a-8

Perfect score: 4078
Sequence: 1 MTGIAASFNTCRFGCGG.....KALETDSVSGVSKQKQKL 776

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New:*

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2: /SIDS/ptodata/1/pubppa/US06_NEW_PUB.pep:*
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4: /SIDS/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
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7: /SIDS/ptodata/1/pubppa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	661	16.2	243	7	US-11-072-512-2404 Sequence 2404, Ap
2	176.5	4.3	1142	7	US-11-087-099-3831 Sequence 3831, Ap
3	153.5	3.8	1279	6	US-10-793-626-3188 Sequence 3188, Ap
4	147	3.6	2228	6	US-10-511-096-2 Sequence 2, Appl1
5	147	3.6	2230	6	US-10-511-096-4 Sequence 4, Appl1
6	147	3.6	2250	6	US-10-511-096-6 Sequence 6, Appl1
7	147	3.6	2252	6	US-10-511-096-8 Sequence 8, Appl1
8	140.5	3.4	5406	6	US-10-995-561-774 Sequence 774, App
9	139.5	3.4	1085	7	US-11-087-099-11646 Sequence 11646, A
10	138.5	3.4	2896	7	US-11-124-368A-306 Sequence 306, App
11	138.5	3.4	2896	7	US-11-124-367A-434 Sequence 434, App
12	135	3.3	3803	6	US-10-995-561-773 Sequence 773, App
13	135	3.3	3960	6	US-10-995-561-771 Sequence 771, App
14	135	3.3	5335	6	US-10-995-561-777 Sequence 777, App
15	135	3.3	5415	6	US-10-995-561-779 Sequence 779, App
16	135	3.3	5464	6	US-10-995-561-775 Sequence 775, App
17	135	3.3	5935	6	US-10-995-561-776 Sequence 776, App
18	134.5	3.3	1299	6	US-10-204-639-70 Sequence 70, Appl
19	131.5	3.2	4384	6	US-10-821-234-1120 Sequence 1120, Ap
20	131	3.2	2426	7	US-11-203-806A-11 Sequence 11, Appl
21	128.5	3.2	2910	6	US-10-330-773-39 Sequence 39, Appl
22	128.5	3.2	3256	7	US-11-124-368A-304 Sequence 304, App
23	128.5	3.2	3256	7	US-11-124-367A-432 Sequence 432, App
24	128	3.1	798	6	US-10-514-531-2 Sequence 2, Appl1
25	124.5	3.1	1347	7	US-11-087-099-5370 Sequence 5370, Ap

26	122.5	3.0	1160	7	US-11-087-099-6576 Sequence 6576, Ap
27	122.5	3.0	2668	7	US-11-124-368A-215 Sequence 215, App
28	122	3.0	1033	7	US-11-087-099-8833 Sequence 8833, Ap
29	121	3.0	2251	7	US-11-183-203-30 Sequence 30, Appl
30	121	3.0	2351	7	US-11-244-087-3 Sequence 3, Appl1
31	121	3.0	2351	7	US-11-267-631-49 Sequence 49, Appl
32	120	2.9	943	6	US-10-475-204-34 Sequence 34, Appl
33	119.5	2.9	599	6	US-10-995-561-812 Sequence 812, App
34	119.5	2.9	2897	6	US-10-499-715-2 Sequence 2, Appl1
35	119.5	2.9	8746	7	US-11-098-688-10232 Sequence 10232, A
36	119	2.9	760	7	US-11-087-099-1634 Sequence 1634, Ap
37	119	2.9	1346	7	US-11-060-005-2 Sequence 2, Appl1
38	119	2.9	1609	7	US-11-087-099-4181 Sequence 4181, Ap
39	118	2.9	463	7	US-11-096-568A-1230 Sequence 1230, Ap
40	118	2.9	464	7	US-11-096-568A-1229 Sequence 1229, Ap
41	118	2.9	480	7	US-11-096-568A-1228 Sequence 1228, Ap
42	118	2.9	915	7	US-11-087-099-6117 Sequence 6117, Ap
43	118	2.9	1037	7	US-11-087-099-6333 Sequence 6333, Ap
44	117	2.9	2096	6	US-10-995-561-606 Sequence 606, App
45	117	2.9	2351	6	US-10-995-561-608 Sequence 608, App

ALIGNMENTS

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RESULT 1
US-11-072-512-2404
Sequence 2404, Application US/11072512
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: MAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT FILING DATE: 2005-03-07
CURRENT APPLICATION NUMBER: US/11/072,512
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2404
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2404
Query Match 16.2%; Score 661; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTGIAASFNTCRFGCGGHPPLADLTHIEDNHTDPRVLEKQELQOPTVVALSY 60
DB 1 MTGIAASFNTCRFGCGGHPPLADLTHIEDNHTDPRVLEKQELQOPTVVALSY 60
QY 61 INRFMTDAAREOBSLKKKIQPKLSLTLSSSVSRGNVSTPPRHSSGSLTPPTPTPSS 120
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Db      61  INFMPTDAAREBESLKKKIOPKLSLTLSSVSGNVSTPRRSSGSLTPVTPITPSS 120
Qy      121  SFRSSTPT 128
Db      121  SFRSSTPT 128

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RESULT 2

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US-11-087-099-3831
; Sequence 3831, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3831
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-087-099-3831

```

Query Match 4.3%; Score 176.5; DB 7; Length 1142;

Best Local Similarity 20.8%; Pred. No. 5.4e-05; Indels 213; Gaps 35;

Matches 152; Conservative 102; Mismatches 264;

```

Qy      41  DPRVLEKQELQOP-----TYVALSTYINRPMTDAAAREBESLKKKIOPKLSLTLSS-SVS 93
Db      337  DEPGI-KBKREPGANAKETLVALLY--RFKCDT---QKELIKQOQVKRQSISSVS 389
Qy      94  RG-NVSTTP-----RHSSGSLTPPTPTPT-----TPSSFRSSTPTPTPTPTPTPTPT 140
Db      390  PSKVVSTTPQRRNRRESLISVTSSRKRPISFNKFTASSASSNLTTPGSSKRLSKNPSK 449
Qy      141  NLAFIFLHRTLYVSHSRNRTNI--KRTEKVDMDLSTVEKMKGEOS-----187
Db      450  KKLSTIVNOSPTTPAS-RNGASVINEKQKQASISTTKKQKRSRSIKRMSLIPSMK 508
Qy      188  HSLSAHLQLTFTGFPHKNDKPSNSEQNSVTLVLVAVK-----CHKRKDVSC 238
Db      509  RESVTTLMSTYAKLAEDDMEYIEKETKTSNFAFLIDEIFEYEKQIRKEKEHLER 568
Qy      239  PIQVPTG-----KQVPL-IPPLNQ-----258
Db      569  KYREAKARELEERRRQKEKERARKLLEKEDLKRQOEELKQIEIDISLQOEELSKHKE 628
Qy      259  -TKGNPPLAVSNEFEPNSHVKYSLLFR-----VTRPGRRFNGMINGETNENI 311
Db      629  EKLDGNIRISAPWNEEKINHLVDIDILRRNSLQTRPVSRIDPGIMSSPTIEEV 688
Qy      312  DVNEELPARRKRRRDEKTFVAQM-----TVFDKRRRLQLLDGEYE--VAMQEN-EE 361
Db      689  SPVE--PKRTENRELTTEKKILETIRSKFLGSSFNIDKELKSKVEYPSIIAPQRLSEE 746
Qy      362  CPISKKRATWETLI--DGKALPPEF--TSGQPTLOFTLRMGETNDKSTAPLAKLAT 416
Db      747  RIVSDSNDGYESILPLPDGNGVSQLKQSTATTAPVSDGRLLKISE-----IRVQFT 798
Qy      417  RNSESLHQENKPGSVKPTQTLAVESLTTLDLQTRKEKQTPENRQKRLIFVQFLVNNNR 476
Db      799  RKRHRHSESNNKRLSV--LSMTSTYESFTNIVDILKGNLNVNNOQSRI-----845
Qy      477  QCTEARDLDHCPWCTLNCRLKLSLKLKLGHSRFFINYYVHPKGRDIVSINECYDGSY 536
Db      846  PTERSDAD-----SEFLFE-----TVAE--BAEY 867
Qy      537  AGNPQDIHR-----QPGFA--PSRNGVVKTPPTTHIIVCRPKRTKMSME 579
Db      868  TGNSSNDERLYDVGDSTIKDKSALKLNFAFDRFNGSNEAKQTDNLHLPLPLNGDNLRLK 927

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Qy      580  FLESEDEVEOQRTYS-----SGHNRLYFHSDTCLPLRPOEMVSEDEKDPEN-----628
Db      928  -QNSQEGDQAHKPKISMIPESGSSS---HTE-----KEFNNEKEKEKKPEQHKEQEQ 976
Qy      629  -LREKTTIQIE 638
Db      977  EKREKVVDDME 987

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RESULT 3

```

US-10-793-626-3188
; Sequence 3188, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3188
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3188

```

Query Match 3.8%; Score 153.5; DB 6; Length 1279;

Best Local Similarity 17.5%; Pred. No. 0.0034; Indels 211; Gaps 35;

Matches 141; Conservative 146; Mismatches 310;

```

Qy      30  IEHIEDNHIDTPRVLEKQELQOPTYVALSTYINRPMTDAAAREBESLKKKIOPKLSLTLSS 89
Db      528  LEKINNIOPTQKTNKAEINDKAQEOILQINN--TPDATBEKQATNRVNGAQAIOAQ 586
Qy      90  SSVSRGNVSTPPRHSGSLTPPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 149
Db      587  -----NINN--AHSQEVNESKTSNIATIKSVQPVNIKPTAINGSLTQEA-----630
Qy      150  RLLTYVSHNSRNIRK-----TFKVDMLSKVEKMGEOESHLSAH-----LQFT 199
Db      631  NQKTLIGNQMATDDEKAKOLVYQKLNQLOKIHESIQDQNVQVNAQAATAIKLI--688
Qy      200  GFPHKNDKPSNSEQNSVTLVLVAVKCHKRKDVSCPIRQVPTGKQVPLIPDLNQT 259
Db      689  -----NANAHKQDAIN--ILTNLAESKSDIRA--NQDATTEKNTAIGSIDDT 734
Qy      260  KPGNPSLAVSSNEFEPNSHVKYSLLFRVTRPGRRFNGMING-----305
Db      735  -----LAQARNNINGANTNALVDENL-----EDKQKQRLQVLSVQTKYQAKADIAQ 782
Qy      306  -----ETNENIDVNEELPARRKRRR-----DGEKTFVAQMTPVD-KNRLQLLDGE 351
Db      783  IGOQRSTIDQNOATTEBEKQOALERLNOETNGVNDIOAALANQVTDKNNILLETIRNV 842
Qy      352  YEVAQMEBECPISKRATWETLIDGKRLPPPTFGQPTL-----QTLRWGTENDKSTA 408
Db      843  EPIVIVKPRANEIIRKKAABQTLINQ-----NQDATLEBKQIALGLGEVKQEBALN 894
Qy      409  PIKPLATRNSESLSQEN-----KPGSVKPTQTLA--VKSLLTLDLQTRKEKQTPENRQK 462
Db      895  QVSQ--AHSNNDVKIYENNGIAKISEVHPETIIKRNKQOIEBDAQS--QIDTINAN---947
Qy      463  LRIFQVFLVNNNRQCTEARDLDHCPWCTLNCRLKLSLKLKLGHSRFFINYYVHPKGA 522
Db      948  -----NKSINNEKSAIID-----RVNAKIDAI-----NNTITNATTT 979
Qy      523  RIDVSINECYDGSYAGNPQDIHRQPGFAFRNGPVKRTPTTHIIVCRPKRTKMSMEBLE 582

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Db 980 QV---VN---DAKNSNTSISQILPSTA-----VK-----TWALALAEAKNAKAIIOQ 1023
QY 583 SEDGEVOOQRTYSSGHNRLYFHSDDTCLPLRPOEMEVDSDEKDEPWLREKTTIOI----- 637
Db 1024 TNATATREKESEANAKVDRL-----OEBADANILKAHTTDEVANNIKN 1064
QY 638 BEFSDVNEGEKEVMKLMNLHVAKHGFIADONMNAHMLFVENYGOKIIR----- 686
Db 1065 QAVONINAVQVEVIKQN-----AKQOLNQ-----PIDNQ-KKIIENTDATTLEKA 1110
QY 687 --KNICRNPMHL---VSNHDPNLISIMSIDAVTKLRMOOKLEKESASPAHEITEE 741
Db 1111 EANRLQNVLTSTDSIEIANVDHNNEVDQALDKARPKIEAIVPOVSKGRDALNAIOEAFNS 1170
QY 742 ONGTANGFSEINSKEKALETDSVGSVK 769
Db 1171 QT-----OEIOKEATNEBKEALNK 1192

RESULT 4
US-10-511-096-2

/ Sequence 2, Application US/10511096
/ Publication No. US20060052280A1
/ GENERAL INFORMATION:
/ APPLICANT: Evotec Neurosciences GmbH
/ TITLE OF INVENTION: Diagnostic and therapeutic use of a Golgi protein for
/ TITLE OF INVENTION: neurodegenerative diseases
/ FILE REFERENCE: P67813US1
/ CURRENT APPLICATION NUMBER: US/10/511,096
/ CURRENT FILING DATE: 2004-10-14
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 2228
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-511-096-2

Query Match 3.6%; Score 147; DB 6; Length 2228;

Best Local Similarity 18.2%; Pred. No. 0.023;
Matches 152; Conservative 148; Mismatches 308; Indels 228; Gaps 36;

QY 30 IEIHEDNHIDDPVLEK-----OELOQPTVALSYINRFMTDAARBOESLKKKIQ 81
Db 330 LEKIDLMMAEKTKILITQLDAKNIIEQLEQDQKGVIAETRKQMETLEMKEEBEIAQLRS 389
QY 82 PKLSLTSSSVSRGNVSTPRHSSGSLPPVTPTPTSSSPRSSSTPTEPTQIYRFLRTN 141
Db 390 RIKQMTTQGEELREQEKESERAAFELEKALSTAQTEBARKKLAEMDEQIKTEKTS 449
QY 142 LIAPFLRRTLTYMHSRNSRTNIKRTPKV-----DMLSKVEKA-----KGBOESHSL 190
Db 450 -----BEERISLQOELSRVQEVVDVWKKSSBEOIATLQKHEKELARKEB---L 496
QY 191 SAHLQLTGTFPHKNDKPSNSENEONSVTLEVL---LVKVCCHKRKQVSCPIROVPYK 247
Db 497 TKKLTQTRERF-----OQOMKVALEKSGSEYIKLSIQEBQOESLALBELBLQK 544
QY 248 KQV-----PLPDLNQTKRGNFPPLAVSSNEFEPSNSHNVKSYSLFVTRPGREFFNGM 302
Db 545 KAILTESENKLRDLQO-----BAETVTRTILLESLSLEKSLQENKQNSDL 590
QY 303 ---INGETNENIDVNEELPARKKRNDEGEKTFVAQMTVPDKNRRLQLLDEYEVAMQEM 359
Db 591 AVHLAEAKNKH---NKEITVWVBKHKTLESLAKHQDQDALM---TEKLYVLKQOYQTEMEKL 645
QY 360 -EECPISKRAWTETILQDKRLPPEPTSGQPTLQFTLRWGETNDKSNAP-----AK 412
Db 646 REKCGOEK-----ETLLDKKEI-IFQAHLE-----ENNEKTELEKIDVQOTELE 687
QY 413 PLATNNSSL---HOENKRGVYKPTQTIATVKSLLTTDLQTRKEKQDTPENNRQKAIIFYQF 469

Db 688 SLSSSELSEVLKARHKLBEELSVLKDQTDKMKOELAKNDEOK-----NHHQOQVDSIIE 742
QY 470 LYNNNTROQTEARDLHPCWCTLNCRKLYSLI-----KHKLCHSRFIRNYVYHPRGARID 525
Db 743 HEVSTQRTKALKDDQIN-----QLELLKERDKHLK-----EHOAHVENLEAD 785
QY 526 VSINECYGSGYAGNQDIIHQGFAPFASRNGPVKRTPIITHLVCRPKRTYASSEF----- 580
Db 786 IKRSE-GELQQSALDVPFGYSQSA-----TH-----EQRTAYEEOQLAQLOQ 826
QY 581 ---LESED-----GEVBOQRTYSSGHNRLYFHSDDTCLPLRPOEMEVDS-----EDEK 624
Db 827 KLIDLETERILITTKQAVAEAKQ-----KDVCTEIDAKHTIGVODIMQOLEKQN 874
QY 625 DEWIREKTIQIEEFSVNBSEKEVMKLMNLHVAKHGFIADONMNAHMLFVENYGOKI 684
Db 875 SEMEOKVASLTQVVE-SKLEIDENKQEOBQOTKQILVEKENNITL--QNRQOKKEIEITQKL 931
QY 685 IKKNLCRNPMHLVSMHDPNLISIMSIDAVTKLRMOOKLEKESASPAHEE----- 737
Db 932 SAKK-----DSIHILN-----BEYETKFNQOEKMKKAKVQAKAKMEETLKKLL 975
QY 738 -----ITBEONGTANGFSEINSKEKALE-----TDSVSGVSKQSKQ 774
Db 976 DQEAUKKELENTA---LELSQEKQFNAKMLEMAQANSAGISDAVSRLETNQKQ 1028

RESULT 5
US-10-511-096-4

/ Sequence 4, Application US/10511096
/ Publication No. US20060052280A1
/ GENERAL INFORMATION:
/ APPLICANT: Evotec Neurosciences GmbH
/ TITLE OF INVENTION: Diagnostic and therapeutic use of a Golgi protein for
/ TITLE OF INVENTION: neurodegenerative diseases
/ FILE REFERENCE: P67813US1
/ CURRENT APPLICATION NUMBER: US/10/511,096
/ CURRENT FILING DATE: 2004-10-14
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 2230
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-511-096-4

Query Match 3.6%; Score 147; DB 6; Length 2230;

Best Local Similarity 18.2%; Pred. No. 0.023;
Matches 152; Conservative 148; Mismatches 308; Indels 228; Gaps 36;

QY 30 IEIHEDNHIDDPVLEK-----OELOQPTVALSYINRFMTDAARBOESLKKKIQ 81
Db 330 LEKIDLMMAEKTKILITQLDAKNIIEQLEQDQKGVIAETRKQMETLEMKEEBEIAQLRS 389
QY 82 PKLSLTSSSVSRGNVSTPRHSSGSLPPVTPTPTSSSPRSSSTPTEPTQIYRFLRTN 141
Db 390 RIKQMTTQGEELREQEKESERAAFELEKALSTAQTEBARKKLAEMDEQIKTEKTS 449
QY 142 LIAPFLRRTLTYMHSRNSRTNIKRTPKV-----DMLSKVEKA-----KGBOESHSL 190
Db 450 -----BEERISLQOELSRVQEVVDVWKKSSBEOIATLQKHEKELARKEB---L 496
QY 191 SAHLQLTGTFPHKNDKPSNSENEONSVTLEVL---LVKVCCHKRKQVSCPIROVPYK 247
Db 497 TKKLTQTRERF-----OQOMKVALEKSGSEYIKLSIQEBQOESLALBELBLQK 544
QY 248 KQV-----PLPDLNQTKRGNFPPLAVSSNEFEPSNSHNVKSYSLFVTRPGREFFNGM 302
Db 545 KAILTESENKLRDLQO-----BAETVTRTILLESLSLEKSLQENKQNSDL 590
QY 303 ---INGETNENIDVNEELPARKKRNDEGEKTFVAQMTVPDKNRRLQLLDEYEVAMQEM 359
Db 591 AVHLAEAKNKH---NKEITVWVBKHKTLESLAKHQDQDALM---TEKLYVLKQOYQTEMEKL 645

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QY -----BECISKRBAWTEIITDCKRLBPREFPBGQPILOTJLAWTEGNDKSTARI-----AK 412
Db REKCOEK-----ETILKCKEI-IFPAHE-----BANEETLEKLVKOTELE 687
QY 413 PLATENSESL---HOENKPGSVKPTOTIAVKESLTTDQTRKEKOTPENROKRLIFYOF 469
Db SLSSELSBYLKBARKHLEELSVLKODTDMMKQGLYAKMBDOK-----NHHQOQVDSIIE 742
QY 470 LYNNNTROOTEARDDLHCWCITLNCRLKYSLL---KHLKLSRIFPNTVHPKCARID 525
Db 743 HEVSIORTERKALKDOIN-----QLEILLKERDKHLK-----EIOAVENILEAD 785
QY 526 VINEECYDGSYANPOPIDIRORPGFAFSRNGPVKRTPIIHLVCRPRKTRKASMEGF-----580
Db 766 IGRSE-GEIQOASAKLIDVQSYOSA-----TH-----EOTRAYEQLAQLOQ 826
QY 581 ---LESED-----GEVEOQRTYSSGHNRLYFHSDTCLPLRPOEMEYDS-----EDEK 624
Db 827 KLIDETERILLTKQVAEVAOK-----KDVCTELDAHKIQUVDLMQOLEKON 874
QY 625 DEWILREKITIIEEFSODNEGEKVEYMKLNLVHMHGFLADONMHACMLFVANTGOKI 684
Db 875 SEMEOQVNSLTVOYE-SKLEDGKKEBOQTKOILVERKENML-OMEBQCKEJILITOKL 911
QY 685 IKKONLCRNFMHLVSNMDFNLISIMSIDRAVTYLRREMOQKTELEGESASPANEE-----737
Db 932 SAKK-----DSIHILN-----BEYETFKNOQEKMEKVKOKAKEMOETLKKKL 975
QY 738 -----ITBONGTANFSRINSKEKLE-----TDSYGVGSOKSKO 774
Db 976 DOBAKTKIKKELNTA---LELSQCKEOPNAKMTLMAOANSAGISIDAVSRLETNOKO 1028

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RESULT 6
US-10-511-096-6
; Sequence 6, Application US/10511096
; Publication No. US20060052280A1
; GENERAL INFORMATION:
; APPLICANT: Evotec Neuroscience GmbH
; TITLE OF INVENTION: Diagnostic and therapeutic use of a Golgi protein for
; TITLE OF INVENTION: neurodegenerative diseases
; FILE REFERENCE: P67813US1
; CURRENT APPLICATION NUMBER: US/10/511,096
; CURRENT FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 2250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-096-6

```

Query Match	3.6%	Score 147	DB 6	Length 2250
Best Local Similarity	18.2%	Pred. No. 0.023		
Matches 152	Conservative 148	Mismatches 308	Indels 228	Gaps 36

```

QY 30 IEHIEHNHLDTPRVEK-----OELOQPPYVALSYNRMPTDPAAREOSLKKKIQ 81
Db 352 LEKIKDILHAETKLTITOLDKANLIEQLEODKGWIAETKROMHETLEKKEBIAORS 411
QY 82 PKLSLTSSSVSKGNSTPPRHSGSLTPPVPPTPIPPSSFRSSTPEPTQYRFLATRN 141
Db 412 RIKOMTQOEBELREQEKESERAFEELEKALSTAOKTEERARKLXKAMDEQINTIETSE 471
QY 142 LIAPFLHRTLTYMHSRNSRTNKKRTFKY----DDMTSKVEKM-----KGEQESHSL 190
Db 472 -----EERISLQOELSRVQOEVDVMKSSSEOIAKLTQKHEKELARQE-----L 518
QY 191 SAHLQUTTFQPFHNDKPSNSNEONSATLEVL---LVVCHKKRQDVSCPIRQVPTGK 247
Db 519 TKKLOTREREF-----QEQMKVALEKSGSEYLKISQKEQOESLAEELELOK 566

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QY      QOV-----PLPDLNQTGRGNFPPLAVSANSNEEPNSHHVKSYSLLFRTRTPORBERNGM 302
Db      KAILTESENKRIKDLOO-----EAYTRYRRLLESLSLEKSLQENKNOSKDL 612
QY      303---INGETNENDIVAEELPARRKRRREDEGEKEFVAQMFTVPFDNRRLQLLDGEEVAMQEM 359
Db      AVHLEAKNKH---NKEITWAVEKKHTLESLSKHQQDML--TEKLQVLKQOVTMEKX 667
QY      360-EECPISKRKAWEITLIDGKRLPRPETSSQGFTLOFTLMGTENDKSTAPI-----AK 412
Db      REKCEQEK-----ETLKDKEI-IFQHAIHE-----ENNKTLEKLDVKOTELE 709
QY      413 PLATANGSSL--HOENKPGSVKPOTIATVESLTDDQTRKEXOTPNENROKLRIFYOF 469
Db      710 SLSELSEYLARAHLEBELSYLKDQOTRMKOLEARKMBOK----NHQOOVSIIKE 764
QY      470 LYNNTROOTEARDLHCPCWTCLNCRKLYSL---KHILCHSRPIFNVVYPKARIID 525
Db      765 HEVSIQRTTEKALKDOIN-----OLELLEKEDKHLK-----EHQAHEVLEAD 807
QY      526 VSINECYGSYAGNPODIHROPGFAPSRNGPVKRTPTITHLVCRPKRTASMSF----- 580
Db      808 IKRSE-GELOQASALDVQSYOSA-----TH-----EQTRAVERQLAQLOQ 848
QY      561 ----LESD-----GEVEOQRITYSSGHNRLYFHSDPTCLPRPOMEVDS-----EDEK 624
Db      849 KLIDLETIRILLTKOVAEVEAOK-----KDVTELDANHIQVDIMLOOLEKN 896
QY      625 DPEMLREKITIOIEESPDVBEKEKEVMKLMNLHWKGFIADONMHACMLFYENTGOKI 684
Db      897 SEMEKVKSILTVOYE-SKLEDGNKQOEQRKOLIVERKNMIL--QMRGQKKEILEILOKL 953
QY      685 IKKONLCRNFMULVSMADFNILSIMSIDKAVTLKREMOKLEKGESASPANE----- 737
Db      954 SAKE-----DSIHILN-----BEYETFKNQOEKMKERVKQAKAMEQETLKKKL 997
QY      738 -----ITEFONCTANGFSINSKEKALE-----TDSVGYSKSKSQ 774
Db      998 DOEAUKKELENTA---DELQSKEQFNPAKMLEMAQANSAGISDAVSTRJETNQEQ 1050
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RESULT 7
US-10-511-096-8
; Sequence 8, Application US/10511096
; Publication No. US20060052280A1
; GENERAL INFORMATION:
; APPLICANT: Evotec Neurosciences GmbH
; TITLE OF INVENTION: Diagnostic and therapeutic use of a Golgi protein for
; TITLE OF INVENTION: neurodegenerative diseases
; FILE REFERENCE: P67813US1
; CURRENT APPLICATION NUMBER: US/10/511,096
; CURRENT FILING DATE: 2004-10-14
; NUMBER OF SEQ. ID NOS.: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO. 8
; LENGTH: 2252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-096-8

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Query Match	3.6%	Score 147	DB 6	Length 2252
Best Local Similarity	18.2%	Pred. No. 0.023		
Matches 152	Conservative 148	Mismatches 308	Indels 228	Gaps 36

```

QY 30 IEHIDNHDTPRYLX-----OELOQPTVYALSYINPMTGAARQCSLSKKIQ 81
    | | | | |
Db 352 LEKIDMLMAEKTUJITQIRDAKNUEIQEIQDQKGVIAFTKQMHTELEWKEBEIAQLR 411
QY 82 PULSTLSSVGRGNVSTPRHSSGLTPPVPTPTSSSPSSSTTEPQIYRPLRTN 144
    | | | | |
Db 412 RIKQNTTOGBELREOKESERAPAELEKALSTAQTEBARRLKAKEMBOQITTEITSE 471
QY 142 LIAPFLHRTLTYMGRHSRTNIKRTFY----DMLSKYEM-----KGEQESHSL 190

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Db 472 -----EERISLOELSRVKEVVDVMKKSSEEOIAXLOKHEKELAREOE---L 518
Qy 191 SAHLLOLTFGPFHKNDKSPNSENEONSTLEVL---LVKVGCHKRKDVSCPIROVPTCK 247
Db 519 TKKLOTREREF-----OQOMKALERSGSEYKIOSEKQOBSLBLELOK 566
Qy 248 KOV-----PLIPDLNOKTKGPNFSLAVSSENEFPNSHMKVKSYSLLFRTRPGREBNM 302
Db 567 KALIBRESEKCLADLOQ-----EAEYTRIRILELESSLEKLOENKQOSKUL 612
Qy 303 ---INGETNENIDVNEELPARRKRNDEDEKTFVAMOTVFDKRRRLQLLDGEYVAMQEM 359
Db 613 AVHLBAEKKH---KKEITVMEKHEKTELESLEKQODALM---TEKLOVUKQOYOTEMEL 667
Qy 360 -EECISKKRAWTETLDOCKLPPPETFSQGTLOPTLAWGETNDKSTAPL-----AK 412
Db 668 REKCEOEK-----ETLLKDKKEI-IFQAHLE-----EMMEKTEKLDVQOTELE 709
Qy 413 PLATNNSBSL---HOENKPGSVKPTQTLAVKESLTTDLQTRKCKDTPNENROKRLRIFYOF 469
Db 710 SLSSLESEVLKARHKLBLEBSLVKQOTDKMKQELEKMDOK-----NHQOQVDSIIEK 764
Qy 470 LYNNNTROQTEARDLHCFWCTLNCRKLYSLI---KHKLCHSRPIFNYYVHPKGARID 525
Db 765 HEVSIORTKALKDOIN-----OLELLKERDKHLK-----EHQAHVENTLEAD 807
Qy 526 VSINCYGGSVAGNPODIHROGPAFSNRGPRVKRPITHILVCRPKRTASNSER----- 580
Db 808 IKRSE-GELOQASAKLDVFOYSOA-----TH-----EQTAAYEBOLAOLQO 848
Qy 581 ----LESED-----GEVEOORTYSSGHNRLYFHSDTCLPLRPOBMEVDS-----EDKE 624
Db 849 KLLDLETRILLTKQVAVENAK-----KDVCTELDAKTIQVODLMQOLEKON 896
Qy 625 DPEWLREKTTIIOIEEFSVDNEGEKEVMKLMNLVHKGFADONMNAHMLFVENYQOKI 684
Db 897 SEMEOKVKSILQVYE-SKLEDGKOEQTKQILVEKENMIL--QUREGQKEIEILQOKL 953
Qy 665 IKONLCRPMMLHVSMDPNLISIMSDKAVTKLREMOKLEKGSASANE----- 737
Db 954 SAKK-----DSIHILN-----BEYETKFNQOEKRMKVKQAKAEMOETLKKLL 997
Qy 738 -----ITEONGTANGFSEINSKEKALE-----TDSVSGVSKOSKIO 774
Db 998 DOBALKKELENTA---LELSQEKQFNAKMLMAQANSAGISDAVSRLETNOKEO 1050

RESULT 8
US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-774

Query Match 3.4%; Score 140.5; DB 6; Length 5406;
Best Local Similarity 18.5%; Pred. No. 0.24;
Matches 172; Conservative 133; Mismatches 350; Indels 277; Gaps 37;
Qy 30 IEHIEDNHIDTDPVLEKO-----E 49

Db 1955 VKKLSDPTVASDPGVLOEOLATTKQLOEELAEHQVVEKLOKARDIMEIEGEPAPDRH 2014
Qy 50 LOQPTVVALSTYINRMTPDAARE-----QSLKKKIOP-----KSL 86
Db 2015 VQETDTSILSHQOSLSYSLAESLLOKAIMOSQOSVLSLOIGREVNOLBGKQVS 2074
Qy 87 TLSSSVSGONVTPPRHSGSLTPVTPPTPTSSFSRSTPTPEPO---IYRFLATRNLA 144
Db 2075 SLSSGVIOBALATNKK-----LKODIARQKSLAEATREMTVTRMETDSTT 2120
Qy 145 PIFLHRTLLYMSHRNSRTNKRKTFKVDMLSKV-----EKMG-----EOSHSLIS 191
Db 2121 AAVLOKGLAEVSGREQLCLOQO---EKSSSLKKLLPQAMFPHLSGKLOQFHNENSRMLA 2178
Qy 132 AHLQ---LFTFGPFHKNDKSPNSENEONSV-TLEVL----- 224
Db 2179 SGNQPDDITHEFOIOELNLEMEQOENLDTLEHLVTELSGCFALDLCQHOREVONIR 2238
Qy 225 ---LVKVGCHKGRDVSCEPIROVPTGKVOPLIPDLNOKTKGNFP---SLAVSNEFPBS 277
Db 2239 KDFTELQTVKEREKDASSCOEQLDEFKRLVTFPOKMLKETBGSLPTETMSAVBLEKO 2298
Qy 278 NSHWKVSYSLLFRVTRPGR---REFNGMNGETNENIDVNEELPARRKRNREDEKTFVAO 335
Db 2299 IEHL---KSLDDMAKGTIVBEIN--CKGSLLENIM--ETAPDSQKTDLTE---IQ 2348
Qy 336 MTFVPRKRLQLLDG-----EYEVAMQMBECISKKRAWTETLDOCKL--LPPETFE 386
Db 2349 CDMSVNKLKYEKDGGLVHEROBSLOAILNRMBE--VHKRAVSVLOMLESKEVELKSDAM 2406
Qy 387 SOGPTLOPTLAWGETNDKSTAPIAKPLATNNSBSLHOENKPGSVKPTQTLAVKESLITTD 446
Db 2407 S-SPTKTETVKAQAESNAFLAEL-----BONSPKIOK-----VKEALAGL 2446
Qy 447 LOTREKEDTPN---ENROKRLIFYOFLYNNNT-----ROQTEARDLHNC----- 487
Db 2447 LVT-----YPRSQAEKNMKKIQBELNSMRERATETVARQOLESASHLACFOAAESQL 2501
Qy 448 -PWC-----TLNCRKLYSLKHLKLCCHSRPIFNYYVHPKGARIDVSI 528
Db 2502 RFWMEKELMAGVLGPLSIDPMLNAOK-----QOVCPMLKEFARROQHEO-----L 2549
Qy 529 NECVDGSVAGNPODIHROGPAFSNRGPRVKRPITHILVCRPKRKASMSERLSEDEBV 588
Db 2550 NEAOGIITG-----PGVUSLSTQOVKE-----LOSINOQWVELTDLNRSISOI 2595
Qy 589 EQORTYSSGHNRLYFHSDTCLPLRPOBMEVSEDEKDEPWLREKTTIIOIEEFSVDNEGEK 648
Db 2596 DOALVKSQYOELLODSEKRVAGQRLSVGSALSTOPEAVAKQ-----OLEETSEIRSDLE 2651
Qy 649 EVMKLMNLVHKGFADONMNAHMLFVENYQOKI IKONLCRPMMLHVSMDPNLISI 708
Db 2652 QLD-----HEVKE---AQTLCDSELVILGEQYLDLCKRL-ETVALPLQGLJDLAADR 2702
Qy 709 MSIDKAVTKLREMOK-----KLEKGSASPAHEITEBONG 744
Db 2703 NRELQALASTQOFQOMDELTMTWLDKQSOQAKNCPIASAKLERLOSULOENEBEFQKSLNQ 2762
Qy 745 TANGFSEINSKEKALETDSVSGVSKOSKOKL 776
Db 2763 HSGYEVIVVAGESILLVPPGEBKRTIQNDL 2794

RESULT 9
US-11-087-099-11646
; Sequence 11646, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450) B EP
; CURRENT APPLICATION NUMBER: US/11/087,099

; CURRENT FILING DATE: 2005-03-22
 ; NUMBER OF SEQ ID NOS: 12464
 ; SEQ ID NO 11646
 ; LENGTH: 1085
 ; TYPE: PRT
 ; ORGANISM: Schizosaccharomyces pombe
 US-11-087-099-11646

Query Match 3.4%; Score 139.5; DB 7; Length 1085;
 Best Local Similarity 20.1%; Pred. No. 0.03; Mismatches 239; Indels 153; Gaps 28;
 Matches 121; Conservative 90;

QY 209 SPENSEONSVLE-VLVYCHKRRKDVSCPIRQVPGKQVPLIPDLNQTGKGFPSL 267
 DB 162 SPNS--VQNNMNLNTVALGSSSTSSKK- - - - - KKKKANSASL 200
 QY 268 AV-SSNEFEPNSHMVKSYSLLFRVT-RPGK--REFYGM-NGETNENIDVNEELPARRK 322
 DB 201 NVDDODDFE- - - - - QVSTDAITYRNGQALSYNGSVROASMMNNNNNNKSKDIWS 253
 QY 323 RNREDGKTFVAQMTVADKRRRLQLDGEYEVAMQEME- - - - - CPI-SKKRATWETI 374
 DB 254 SNTERRQIRREFWLSSEERR-SLVKVEKAVLQKKEQOKTSCSCVGRKRLAIEB 312
 QY 375 LDGKRLPPETFSQGPFLQFLRWGTETN- - - - - DKSTAPIAK- - - - - PLATFNS 420
 DB 313 LEVLVAYYELQYANICQNLANTESVNASDGSQKGIISDPSKLSTPLNNVPSK 372
 QY 421 SLHOENKPGSVKPTQITAVESL-TTDLQTRKEKOTPNENRQKRLIFYOFLYNNNTROOT 479
 DB 373 SLNDITQDELINSSNDVDDEVLETSL- - - - - EKVDNQ- - - - - EFVTSISNGNOT 420
 QY 480 EARDLHCPWCTLNCRKLYSLKMLKLCBSRFIFNYVYHKGARIDVINECYDGSYAGN 539
 DB 421 -LEDTSHSPOTOPFPQPSKADKNSYHSDLYN- - - - - GSSLTVK- - - - - GGLITV 468
 QY 540 PODIHRQGFAPFARNPGVKKRPTTHILVCRPKTKASMSFLESEDEVEQORTYSSGN 599
 DB 469 ADDLKNNDG- - - - - - - - - - - KKFIEEMEDLARRMQREDNSN 499
 QY 600 RLYFHSDTCLPLAPQEMVDSDEKDEPMLEKTIIOIEFSDVNEGEKVMKMLHVM 659
 DB 500 - - - - - FHEP- - - - - ELYESGLEDEDEDEDE- - - - - DVDBEDLDM- - - - - 531
 QY 660 KHGFADNQNKAHMLFVENYGOIKIKNLCSNFMHLVSMHDPNLSIM- - - - - SLDK 713
 DB 532 - - - - - TDEQMEGRFPQIPARLFQGRVLQAVREYVAQORQAKLLEIEENKRRQER 586
 QY 714 AVTLREMOCKLEKGSASPANEETEEQNGTANGFSEINSKEKALETDSVGVSKQSK 773
 DB 587 ELKIREKEKKRDKKQKLAKKE- - - - - BRORREABRLAE-QAQKALEAKRQEBARKKRE 643
 QY 774 OKL 776
 DB 644 ORL 646
 RESULT 10
 US-11-124-368A-306
 ; Sequence 306, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; APPLICANT: May Luke
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; FILE REFERENCE: C0001524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; PRIOR FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,845
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/625,936

; PRIOR FILING DATE: 2004-11-09
 ; NUMBER OF SEQ ID NOS: 21112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 306
 ; LENGTH: 2896
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-124-368A-306

Query Match 3.4%; Score 138.5; DB 7; Length 2896;
 Best Local Similarity 18.1%; Pred. No. 0.14; Mismatches 285; Indels 277; Gaps 35;
 Matches 149; Conservative 113;

QY 12 NTCRFG- - - - - GCGHPETLADLIEH- - - - - IEDNIDDPVLEKQELQOPTVAL 58
 DB 25 STCLFGRGIECOLRIGLPVVSQKHCKIEIHQEALIHNSSTNPQVNSVIDEPRVLRN 84
 QY 59 SYINRPMTDAREQESLK- - - - - KKIQPKSLTSSSVSGNVSTPPRH- - - - - 104
 DB 85 GDVITTIIDSPRYENSLQSGRSTFPRKIREQ- - - - - BPARRVRSFSSDPESDGIPL 141
 QY 105 - - - - - GGLTPPV- - - - - TPPTPSSFRSSTPTEPTQIYRFLRNLIAPIFLHRTL 153
 DB 142 KRRVSGHLRBELEFENLPPVTPDK- - - - - RGEAPL- - - - - 174
 QY 154 YMSHRSTRNIRKT- - - - - FKYDMLSKVERK- - - - - GEQESHLSAHLQLTFTGFPHKNDK 207
 DB 175 - - - - - XKSLVMTTPVLKIIKEQPPSGKQSSG- - - - - EIHVEVKAQSLVSPRA 222
 QY 208 SPENSEONSVLEVLVYCHKRRKDVSCPIRQVPGKQVPLIPDLNQTGKGFPSL 267
 DB 223 PSPRK- - - - - - - - - - - TPVADQRR- - - - - SCTAPASSKSGTE-VPKRGKSGMLPSK 267
 QY 268 AVSNEFEPNSHMVKSYSLLFRVTRPGRREFNGMNGSTNENIDVNEELPARRKNRD 327
 DB 268 RVISRSQHDIIQMTCS- - - - - KRSGASEALIV- - - - - 297
 QY 328 GEKTFVAQMTVPDKRRRLQLDGEYEVAMQEMECPI-SKKRATWETILDGKRLPPETPS 387
 DB 298 -AKSMADVYKLGAKQVQTVIKHGPPQSMNKKQRRATPKK- - - - - PVGEVNS 344
 QY 388 QGFTLOFLRWGTETNDSKTAPIAKPLATRNSESLHOENKPGSVKPTQITAVESLTTDL 447
 DB 345 - - - - - QFS- - - - - TGHANSPCTIIIGK- - - - - AHTEKVVPPARP- - - - - 373
 QY 448 QTRKEKOTPNENRQKRLIFYOFLYNNNTROQTEARDL- - - - - HCPWCTLNCR 495
 DB 374 - - - - - YRLANFISQKMDFKEDLGIAEMFTPVKEQPOLSTC- - - - - 413
 QY 496 KLYSLKHLKLCBSRFIFNYVYH- - - - - PKGARIDVINECYDGSYAGNPQDIHRQGFAPFR 553
 DB 414 - - - - - HIAISSENLKQFGTDSGEBPLLPESSEFGANVFSAQNAKQPSDKCSA 466
 QY 554 NGPVKRTPIYH- - - - - ILVCRPKTKASMSFLESEDEGEVEQORTYSSGHNRLYFHSDTCLPL 611
 DB 467 SPFLRQCIRENGVNAKTPRNTYKMTSLTETKSTDETPESKTYVSTAN- - - - - RSGRSTEB 521
 QY 612 RP-QEMEVDSDEKDEMLREKTIIOIEFSDVNEGEKVMKMLHVMKHGFIANDNM 670
 DB 522 RNIQKLPVESK- - - - - EETNIVE-CLIKRQKATL- - - - - LQORREGMKIEIRP 568
 QY 671 HACMLFVENYGOIKI-KKMLCSNFMHLVSMHDPNLSIMSIDKATYKLRMOCKLEKE 729
 DB 569 - - - - - FETTKENIEKEN- - - - - - - - - - - DE- - - - - IKKAMRSTRWQ 596
 QY 730 SASPANE- - - - - ETEBQNGTANGFSSINSKEKALETDSVSG 766
 DB 597 KCAPMSDLTDLKSLPPTELMKDARQONLQODHAKAPKSEKG 640
 RESULT 11
 US-11-124-367A-434
 ; Sequence 434, Application US/11124367A


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/ Publication No. US20060024700A1
/ GENERAL INFORMATION:
/ APPLICANT: Michele Cargill
/ APPLICANT: Hongjin Huang
/ TITLE OF INVENTION: Genetic Polymorphisms Associated with
/ FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
/ FILE REFERENCE: CL001519.ORD
/ CURRENT FILING DATE: 2005-05-09
/ PRIOR FILING DATE: 2004-08-09
/ PRIOR APPLICATION NUMBER: US 60/568,846
/ PRIOR FILING DATE: 2004-05-07
/ PRIOR APPLICATION NUMBER: US 60/582,609
/ PRIOR FILING DATE: 2004-06-25
/ PRIOR APPLICATION NUMBER: US 60/599,554
/ PRIOR FILING DATE: 2004-08-09
/ NUMBER OF SEQ ID NOS: 34460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 434
/ LENGTH: 2896
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-11-124-367A-434

Query Match          3.4%; Score 138.5; DB 7; Length 2896;
Beet Local Similarity 18.1%; Pred. No. 0.14;
Matches 149; Conservative 113; Mismatches 285; Indels 277; Gaps 35;

QY 12 NTCRG--GCGLHPTLADLIEH-----IEDNIDDPRLVLEQLQOPRYVAL 58
DB 25 STCLFGRGICEDIRQLPVVSKOKIEIHEQALIHNSSTNPQVNSVDEVPALKH 84
QY 59 SYINFMTDARREBSLK-----KIQPKLSLTSSSVSGNVPSPRH----- 104
DB 85 GGVITIDRSFYENHESLOSGRKSTFPKIREQ--EPARVNSGSSSDSDSGIPL 141
QY 105 -----SGSLTPV---TPPTPSSSFSSSTPTEPTQIYRFLRNLRIADIFLHRTLT 153
DB 142 KRRRVFSGHLRPELFDENLPNTPLK--RGEAPF----- 174
QY 154 YMSHNSRNTNIRKT--FKYVDMLSKVEKMK---GEORSHLSAHLQUTFGFHRKNDK 207
DB 175 -----RRKSLVMTTPVLLKKTIEQOPSGKSGS--EIHVEVKAOSLVISPPA 222
QY 208 PSPNSENEQNSVTLVLLVVCVKRKYDSCPIRQVPTGKQVPLIPDLNQTGKGNFPL 267
DB 223 PSBRK-----TPVASDQRR--SCKTAPASSKSGTQ--VPRKGRKSGNLBPK 267
QY 268 AVSSNEPEPSSNHWKYSYSLFRVTRPGRRFNGMINGETNENIDVNEELPARRRKRED 327
DB 268 RVISIRSGHDLQIMCS-----KRRSGASEANLIV----- 297
QY 328 GEKTVAQMTVDKRRRLQLDGEYEVAMQEMEBECPISKRAWTETIILDKRLPPETFS 387
DB 298 -AKSMADVVKGAQAKOTQTKVIRHGPORSNNKQRBPAPPK-----PVEVNS 344
QY 388 QGPTLQTLMTGFTNDSSTAPIAKPLATRNSESLHOENKPGSVKPTQTIIVKESLTTDL 447
DB 345 -----QFS---TGHANSPTIITIGK---AHTEKHVNPAP----- 373
QY 448 QTRKEKQTPNENRQKRIIFYOFLYNNNTROQTEABDL-----HCPWCTLNCR 495
DB 374 -----YRVANFNISNQKMDPFEDLSGLAEMFKTPVKEQPOLSTSC- 413
QY 466 KLYSLKLKLCCHSRFIRNYVH--PKGARIDVSNCEQDSYAAGNPDQIHQOPGFAFR 553
DB 414 -----HIAISNSNLLGKQFOGTDGSEPLLPFSSEFGVFPSSAQVAAKQPSDKCSA 466
QY 554 NGPVKRTPLTH--ILVCRPKRTKASMESEFLESDDEVEOQRTYSSGHNRLVHSTCLPL 611
DB 467 SPTLRQCIKRENGVNAKTPRNTYKMTSLTKTSIDTETBSKTVSTAN-----RSGRSTBF 521
QY 612 RP-QEMEVDSDEKQPEMLREKTTIQIEFSDVNGEKEVKMLMNLHVWKHGFADNQM 670
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DB 522 RNIOKLVPESKS-----EETNTEIVE-CLIKGQKATL-----LQORREGMEKIERP 568
QY 671 HACTLFEVNYGQKI-IKKRLCNPMLHVLVSMDFNLISIMSDKAVTKLRBQOKLEKE 729
DB 569 -----FETTKENIEIKEN-----DE---KKKAKRSRTWQ 596
QY 730 SASPANE-----ETTERONGTANGFSEINSKEXALETDSVSG 766
DB 597 KCAPMSDLDLKSJLDTBLMKQTARGONILQTDIAKAPKSKG 640

RESULT 12
US-10-995-561-773
/ Sequence 773, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 773
/ LENGTH: 3803
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-10-995-561-773

Query Match          3.3%; Score 135; DB 6; Length 3803;
Beet Local Similarity 17.6%; Pred. No. 0.38;
Matches 169; Conservative 133; Mismatches 344; Indels 316; Gaps 36;

QY 30 IEHIEDNIDDPRLVLEQ-----E 49
DB 1955 VEKLSIDTVASDPVLOQLQALTTKQLOBELAENOVPEKQKAVADIHEIBEPAPDRH 2014
QY 50 LQOPRYVALSYINFMTDARRE-----QESLKKIOP-----KLSL 86
DB 2015 VOETDSILHSOSLSYSLSARSLSLOKAIQSGQGSLSLSIGSEVEQNLGKQVS 2074
QY 87 TLSSSVSGNVTSPRHSSGSLTPVTPPTPSSSFSSSTPTEPTQ--IYRFLRNLRI 144
DB 2075 SLSSGVIOBALATNMK-----LKQDIARQKSLSEATREMTVTRMETADSTT 2120
QY 145 PIFLHRTLTYSNHSRNTNIRKTKFVDMLSKV-----EKMKG-----EQRSHSIS 191
DB 2121 AAVLOGKLAIVSQREQLCLQQ--EKESLKLKLLPQAMRPHLSGKIQOPWENKSRMLA 2178
QY 192 AHLQ--LTFGPFHKNKDPSPNSEQNSV--TLEVL----- 224
DB 2179 SGNQPDODITTFPOIQIOLANLEMEDQENLDTLEHLVTESSCGPALDLQHQDRVQNL 2238
QY 225 -----LVVCHKKRKYDSCPIRQVPTGKQVPLIPDLNQTGKGNP--SLAVSSNEPFS 277
DB 2239 KQFTELQTVKEREKDASSCOBQDEFRKLVTFQKMLKETEGSIPPTETSAAELEKQ 2298
QY 278 NSHWKYSY-----SLFVTRPGRRFNGMINGETNENI----- 311
DB 2239 IEHL-KSLDDWMAKGTIVEINCKGTSLEMLMEITARPDAQGKGSILPSSGVSVN 2357
QY 312 -----DVNEELPARRRKREDGEKTFVAQMTVPDKRRLLQLDG-----EYEVAMQ 358
DB 2358 GYHTCKDLTE-----IQCDMSVNLKYKELGGLVHEROESIQALINR 2399
QY 359 MEQCPISKRAWTETIILDKR--LPPEFSGQPTLQTLMTGFTNDSSTAPIAKPLAT 416
DB 2400 MEE--VHKANSVUQWLESKEEVLKSMAMS--SPTKETVVAQAESNAFLAEL----- 2450
QY 417 RNSESLHOENKPGSVKPTQTIIVKESLTTDLQTRKEKQTPN-----ENRQKRIIFYOFLYN 472
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Db 2451 -----EQNSPKIOK-----VKEALAGLVT-----YPSQEAENWKKIOBELNSRWE 2492
Qy 473 NNT-----ROOTEARDLHC-----PWC-----TLNCRKLY 498
Db 2493 RATEVTVARQROLESASHLACFOAAESQLRPWLMEKELMMGYLGPLSIDPNNMLNOK-- 2550
Qy SLKHLKLCGSRPFTFNVVYHPKGAIDVINECYDGSYAGNPQDIIHQPGFAFSRNGPYK 558
Db 2551 ---QOVQFMKEFEARQOHEQ-----LNEAAQOILTG-----PODVSLSSTQVQ 2592
Qy 559 RTPITHLVCRPRTKYSMSFLESEDEGEVQOQRTYSSGHNRLYFHSDTCLPLRPOEMEV 618
Db 2593 KE-----LQSIHQKWTBELTDKLNSSSQIDQAIKVSQYQOELLQDISEKVRAYGVGRLSV 2646
Qy 619 DSEDEKDPWLRKRTITQIEEESDVNGEKEVKMLNLMYMKIGFLADNQMNAICMLFVE 678
Db 2647 QSAISTQPEAVKQ-----QLEETSEIRSDLEOLD-----HEVKE---AQTLCDLSVLIGE 2694
Qy 679 NYGOKIIRKNLCNFMHLVSMDFNLISMSIDKAVTKLEMOQ----- 723
Db 2695 QYKDELKRL-ETVALPLOGLEDLADRINRLQALASTQOQOQMFDELRTWLDKQSQ 2753
Qy 724 -----KLEGESASPANEITEBONGTANGFSEINSKEKALETDSVSVSKQSKQ 774
Db 2754 QAKNCPISAKLEBLOQOLQENEEFOKSLNQHSGSYEVIVAEGSLLSVPPGEEKRTIQN 2813
Qy 775 KL 776
Db 2814 QL 2815

RESULT 13
US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-995-561-771

Query Match 3.3%; Score 135; DB 6; Length 3960;
Best Local Similarity 17.6%; Pred. No. 0.4;
Matches 169; Conservative 133; Mismatches 344; Indels 316; Gaps 36;
Qy 30 IEHEDHIDTPDPRVLEKQ-----E 49
Db 1955 VEKLSITVASDPGVLOEQALATTQOLQBELAHQVPEKIQKVARIMEIEGEPAPDRH 2014
Qy 50 LQOPTVALSYINFMTDAARR-----QESLKKKIQP-----KLSL 86
Db 2015 VQETTDLSLHFGSLSYSLAERSLLQKALAQOSQVQESLESLLQSIGEVQONLEGKQVS 2074
Qy 87 TLSSSRKGVSTPPRRSSSGSLTPPVPTPITSSPSSSTPTETQ--IYRFLRTRLIA 144
Db 2075 SLSSGVIQALATMK-----LKODIAKQKSLKXTRMVTREMTAOSTT 2120
Qy 145 PIFLHRTLVYMSHRNSRTNKRKTFKYDMLSKV-----EKAKG-----EOESHLS 191
Db 2121 AAVLQGLAVSQRFEOQLCLOQ--EKSSLKLLLPQAEFHLISGLQOFMEKSKMLA 2178
Qy 192 AHLO--LTFGFFHKNDKPSNSENQNSV-TLEVL----- 224

Db 2179 SGNOPODITHFPOQIOELNLEMEQOENIDLTLEHLVTELSGCGFALDLCOHQDRVQNL 2238
Qy 225 -----LVKXCHKKRDVSCPIRQVPTGKKQVPLIPDLNQTOKGNP--SLAVSSNEFES 277
Db 2239 KQTELOKTVKEREKQDASSQOQDEFRKLVTPQKMLKETBSIPIPTETSNAKLEKQ 2298
Qy 278 NSHMVKS-----SLFRVTRGRREFGNMGINGETMENT---- 311
Db 2299 IEHL-KSLDDMAKSKTLVEINCKGTSLENLIMETAPDSQOKGSIIPSVGSSGVSV 2257
Qy 312 -----DVNEELPARKNRREDGKTFVAQMTVFQKRLQLLDG-----EYVAMQE 358
Db 2358 GYHTCKDLTE-----IQCMSDVNLKYEKLGVLHERQESLOAILNR 2399
Qy 359 MESCPISKRAWTETLDGK--LPPETFSQOPLQFLBMTGETNDRSTAPIAPLAT 416
Db 2400 MEE--VHKANSTLQWLESKEBYLSMDMS--SPITTEVKAQAEKNKAFLEL----- 2450
Qy 417 RNSESIHOENKPGSVPTQTIAVKESLTTDLQTRKEKQTPN---ENROKLRIYQOFLYN 472
Db 2451 -----EQNSPKIOK-----VKEALAGLVT-----YPSQEAENWKKIOBELNSRWE 2492
Qy 473 NNT-----ROOTEARDLHC-----PWC-----TLNCRKLY 498
Db 2493 RATEVTVARQROLESASHLACFOAAESQLRPWLMEKELMMGYLGPLSIDPNNMLNOK-- 2550
Qy 499 SLKHLKLCGSRPFTFNVVYHPKGAIDVINECYDGSYAGNPQDIIHQPGFAFSRNGPYK 558
Db 2551 ---QOVQFMKEFEARQOHEQ-----LNEAAQOILTG-----PODVSLSSTQVQ 2592
Qy 559 RTPITHLVCRPRTKYSMSFLESEDEGEVQOQRTYSSGHNRLYFHSDTCLPLRPOEMEV 618
Db 2593 KE-----LQSIHQKWTBELTDKLNSSSQIDQAIKVSQYQOELLQDISEKVRAYGVGRLSV 2646
Qy 619 DSEDEKDPWLRKRTITQIEEESDVNGEKEVKMLNLMYMKIGFLADNQMNAICMLFVE 678
Db 2647 QSAISTQPEAVKQ-----QLEETSEIRSDLEOLD-----HEVKE---AQTLCDLSVLIGE 2694
Qy 679 NYGOKIIRKNLCNFMHLVSMDFNLISMSIDKAVTKLEMOQ----- 723
Db 2695 QYKDELKRL-ETVALPLOGLEDLADRINRLQALASTQOQOQMFDELRTWLDKQSQ 2753
Qy 724 -----KLEGESASPANEITEBONGTANGFSEINSKEKALETDSVSVSKQSKQ 774
Db 2754 QAKNCPISAKLEBLOQOLQENEEFOKSLNQHSGSYEVIVAEGSLLSVPPGEEKRTIQN 2813
Qy 775 KL 776
Db 2814 QL 2815

RESULT 14
US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 5335
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-995-561-777
Query Match 3.3%; Score 135; DB 6; Length 5335;
Best Local Similarity 17.6%; Pred. No. 0.61;

Matches 169; Conservative 133; Mismatches 344; Indels 316; Gaps 36;

QY 30 IEHEDNHITDPRVLEKO-----E 49
DB 1863 VEKLSIDTVASDPGVLOEQJLATTQLOEELAEHQVVEKLOKVARDIMEIEGEPADHRH 1922
QY 50 LQOPTVVALSYINRMTJAAARE-----QESLKKKTOP-----KLSL 86
DB 1923 VOETTDSILSHFQSLSYSLAEBSLLOKALAQOSQVQESLBSLQSIGEVONLEBKQVS 1982
QY 87 TLSSSVSKGNVSTPRHSSGSLTPPVTPPTSSFRSSTPEPQO--IYRPLRTNLLA 144
DB 1983 SLSSGVIOEALATNMK-----LKODIAROKSSLEATREMTVTRFMTADSTT 2028
QY 145 PIFLHRTLYMSHRNRTNIRKRTFKVDMLSKV-----EKMKG-----EGBSHSL 191
DB 2029 AAVLOGLKLAESQRFQJLQOO--EKESLKKLLPQAEFHEHLSGLQOFMENNKRMLA 2086
QY 192 AHLQ--LFTGPFHKNKDPSPNSEENQSV--TLEVL----- 224
DB 2087 SGNQRPQDITTHFQOIQELNLEMEQOENLDTLEHLYTELSCGFALDLCQHODRVQNL 2146
QY 225 ----LVVCHKKRQDVCPTRQVPTGKQVPLIPDLNQTGKNFP--SLAVSNBEPES 277
DB 2147 KQFTLQKTVKEREKQDASSCOEQLDBFRKLVTFPKMLKETGSLIPPTETMSAKLEKQ 2206
QY 278 NSHMVKS-----SILFRTPRGRREFNGMNGTENI----- 311
DB 2207 IEHL--KSLDDWASKGLVEBINCKGTSLENLIMETAPDSQKTSILPSVSSVGSVN 2265
QY 312 ----DVNEELPARKRNRDEGEKTFVAQMTVPFKNRRLQLLDG-----EYEVAMOE 358
DB 2266 GYHTCKDLTE-----IQCDMSDVNLKYEKLGVLHERQESLQAIILNR 2307
QY 350 MEECPISKRAATWETILDGKR--LPPFTFSOGPTLOFLRMTGETNDKSTAPIAKPLAT 416
DB 2308 MEE--VHKANSVULQWLESKEEVLKSMQDMS--SPKTETVAKQAQESNAKFLAEL----- 2358
QY 417 RNSESLHQENKPGSVKPTOTIAVKESLTTDLQTRREKQTPN---ENRQKLAIFYOFLYN 472
DB 2359 ----EONSPKIQK-----VKELAGLLVT-----YPSQAEENMKKIOEBINSRWE 2400
QY 473 NNT-----ROOTEARDLHC-----PMC-----TLNCRKLY 498
DB 2401 RATEVTVARQRLAESASHLACFOAAESQLRPMLEKELMVGVLPLSIDPMMLAOK-- 2458
QY 499 SLKHLKLCBSRPFIFNYVYHPKGARIDVINSCEYDGSVAGNPQDIHROGFAFSRNGPYK 558
DB 2459 ----QOVQFMLKEFEARRQOHEQ-----LNEAAQGIILTG-----PGDVSLSSTQVQ 2500
QY 559 RTPITHILVCRPKRTKASMEFLSEBDEGEVBOQRTYSSGHNRLYFHSOTCLPLRQEMEV 618
DB 2501 KE-----LOSINQKMWELTDKLNRSQIDQAIYKSTQYQELLDLSEKRAVAGQRLSV 2554
QY 619 DSEDEKDPWLEKRTITTOIEEFSDVNBEKKEVAKMLNLMVHGFLADQNMHACLFVE 678
DB 2555 QSAISTQPEAVKQ-----QLEETSEIRSDLEQJD-----HEVGE--AQLCDELVLIGE 2602
QY 679 NYGQKIKKNCGRNFMHLVSMHDFNLISIMSIDAVTKLRMQO----- 723
DB 2603 QYIKDELKKRL--ETVALPLOGLEDLAADRINRLQALASTQFOQMFDELRMTLDDKSO 2661
QY 724 ----KLEKGSASPANEITEBQNGTANGSEINSEKKALETDSVGSVQSKQ 774
DB 2662 QAKNCPISAKLERLOSQLOEENEFQKSLNQHSGSYEVIVABGESLILSVPEEKRTLQON 2721
QY 775 KL 776
DB 2722 QL 2723

Sequence 779, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION: Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 779
LENGTH: 5415
TYPE: prt
ORGANISM: Homo sapiens
US-10-995-561-779

Query Match 3.3%; Score 135; DB 6; Length 5415;
Best Local Similarity 17.6%; Pred. No. 0.62;
Matches 169; Conservative 133; Mismatches 344; Indels 316; Gaps 36;

QY 30 IEHEDNHITDPRVLEKO-----E 49
DB 1955 VEKLSIDTVASDPGVLOEQJLATTQLOEELAEHQVVEKLOKVARDIMEIEGEPADHRH 2014
QY 50 LQOPTVVALSYINRMTJAAARE-----QESLKKKTOP-----KLSL 86
DB 2015 VOETTDSILSHFQSLSYSLAEBSLLOKALAQOSQVQESLBSLQSIGEVONLEBKQVS 2074
QY 87 TLSSSVSKGNVSTPRHSSGSLTPPVTPPTSSFRSSTPEPQO--IYRPLRTNLLA 144
DB 2075 SLSSGVIOEALATNMK-----LKODIAROKSSLEATREMTVTRFMTADSTT 2120
QY 145 PIFLHRTLYMSHRNRTNIRKRTFKVDMLSKV-----EKMKG-----EGBSHSL 191
DB 2121 AAVLOGLKLAESQRFQJLQOO--EKESLKKLLPQAEFHEHLSGLQOFMENNKRMLA 2178
QY 192 AHLQ--LFTGPFHKNKDPSPNSEENQSV--TLEVL----- 224
DB 2179 SGNQRPQDITTHFQOIQELNLEMEQOENLDTLEHLYTELSCGFALDLCQHODRVQNL 2238
QY 225 ----LVVCHKKRQDVCPTRQVPTGKQVPLIPDLNQTGKNFP--SLAVSNBEPES 277
DB 2239 KQFTLQKTVKEREKQDASSCOEQLDBFRKLVTFPKMLKETGSLIPPTETMSAKLEKQ 2298
QY 278 NSHMVKS-----SILFRTPRGRREFNGMNGTENI----- 311
DB 2239 IEHL--KSLDDWASKGLVEBINCKGTSLENLIMETAPDSQKTSILPSVSSVGSVN 2357
QY 312 ----DVNEELPARKRNRDEGEKTFVAQMTVPFKNRRLQLLDG-----EYEVAMOE 358
DB 2358 GYHTCKDLTE-----IQCDMSDVNLKYEKLGVLHERQESLQAIILNR 2399
QY 350 MEECPISKRAATWETILDGKR--LPPFTFSOGPTLOFLRMTGETNDKSTAPIAKPLAT 416
DB 2400 MEE--VHKANSVULQWLESKEEVLKSMQDMS--SPKTETVAKQAQESNAKFLAEL----- 2450
QY 417 RNSESLHQENKPGSVKPTOTIAVKESLTTDLQTRREKQTPN---ENRQKLAIFYOFLYN 472
DB 2451 ----EONSPKIQK-----VKELAGLLVT-----YPSQAEENMKKIOEBINSRWE 2492
QY 473 NNT-----ROOTEARDLHC-----PMC-----TLNCRKLY 498
DB 2493 RATEVTVARQRLAESASHLACFOAAESQLRPMLEKELMVGVLPLSIDPMMLAOK-- 2550
QY 499 SLKHLKLCBSRPFIFNYVYHPKGARIDVINSCEYDGSVAGNPQDIHROGFAFSRNGPYK 558
DB 2551 ----QOVQFMLKEFEARRQOHEQ-----LNEAAQGIILTG-----PGDVSLSSTQVQ 2592
QY 559 RTPITHILVCRPKRTKASMEFLSEBDEGEVBOQRTYSSGHNRLYFHSOTCLPLRQEMEV 618
DB 2593 KE-----LOSINQKMWELTDKLNRSQIDQAIYKSTQYQELLDLSEKRAVAGQRLSV 2646

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QY 619 DSEDEKOPWLBREKTTTQIIEBESDVNGEKEVWKLWNHLVWKGFIADNOMHACMLFVE 678
DB 2647 OSAISTOPFAVKQ---OLEETSEIRSDLEOLD---HEVKE---AQTLCELSVLIGE 2694
QY 679 NYGOKIHKKNLGRNFMHLVSMHDFNLLISIMSIDKAVTKLREMQQ----- 723
DB 2695 QYIKDELKRL-ETVALPLOGLEDLAADRINRLQALASTQOFQOMFDELRTWDDKQSQ 2753
QY 724 -----KLEKESASAPNEEITEBQNGTANGFSEINSKEKALETDSVSGVSKQSKQ 774
DB 2754 QAKNCPIASAKLBRLOQOLGENEESFOKSIHQSGSYEVYVAEGESLILSVPPGEEKRTLOV 2813
QY 775 KL 776
DB 2814 QL 2815
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